

UTILITY PATENT APPLICATION TRANSMITTAL

(Only for new nonprovisional applications under 37 CFR § 1.53(b))

Attorney Docket No.		0942.4460002/RWE/BJD
First Inventor		FOX et al.
Title	Methods and Compositions for Cloning Nucleic Acid Molecules	
Express Mail Label No.		

APPLICATION ELEMENTS

See MPEP chapter 600 concerning utility patent application contents.

ADDRESS TO:

Assistant Commissioner for Patents
Box Patent Application
Washington, DC 20231

Fee Transmittal Form (e.g., PTO/SB/17)
(Submit an original, and a duplicate for fee processing)

Applicant claims small entity status.
See 37 CFR 1.27.

3. ☒ Specification [Total Pages 62]
(preferred arrangement set forth below)
- Descriptive title of the invention
 - Cross Reference to Related Applications
 - Statement Regarding Fed sponsored R & D
 - Reference to sequence listing, a table, or a computer program listing appendix
 - Background of the Invention
 - Brief Summary of the Invention
 - Brief Description of the Drawings (if filed)
 - Detailed Description
 - Claim(s)
 - Abstract of the Disclosure

4. ☒ Drawing(s) (35 U.S.C. 113) [Total Sheets 1]

5. Oath or Declaration [Total Pages 2]

- a. ☐ Newly executed (original or copy)
- b. ☒ Copy from a prior application (37 CFR 1.63(d))
(for continuation/divisional with Box 17 completed)

i. ☐ **DELETION OF INVENTOR(S)**
Signed statement attached deleting inventor(s)
named in the prior application, see 37 CFR §§
1.63(d)(2) and 1.33(b).

6. ☐ Application Data Sheet. See 37 CFR 1.76.

7. ☐ CD-ROM or CD-R in duplicate, large table or Computer Program (Appendix)
8. Nucleotide and/or Amino Acid Sequence Submission (if applicable, all necessary)
- a. ☐ Computer Readable Form (CRF)
- b. Specification Sequence Listing on:
- i. ☐ CD-ROM or CD-R (2 copies); or
- ii. ☐ paper
- c. ☐ Statements verifying identity of above copies

ACCOMPANYING APPLICATION PARTS

9. ☐ Assignment Papers (cover sheet & document(s))
10. ☐ 37 CFR 3.73(b) Statement (when there is an assignee) ☐ Power of Attorney
11. ☐ English Translation Document (if applicable)
12. ☐ Information Disclosure Statement (IDS)/PTO-1449 ☐ Copies of IDS Citations
13. ☒ Preliminary Amendment
14. ☒ Return Receipt Postcard (MPEP 503) (Should be specifically itemized)
15. ☐ Certified Copy of Priority Document(s) (if foreign priority is claimed)
16. ☒ Other: Authorization under 37 C.F.R. § 1.136(a)(3)
- ☒ Other: Check No. 29288 in the amount of \$710.00
- ☒ Other: Letter to PTO Draftsman: Submission of Formal Drawings

17. If a CONTINUING APPLICATION, check appropriate box, and supply the requisite information below and in a preliminary amendment, or in an Application Data Sheet under 37 CFR 1.76:

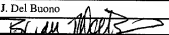
- ☐ Continuation ☒ Divisional ☐ Continuation-in-Part (CIP) of prior application No: 09/134,672
Prior application information: Examiner Johansen, D. Group/Art Unit: 1655

For CONTINUATION OR DIVISIONAL APPS only: The disclosure of the prior application, from which an oath or declaration is supplied under Box 5b, is considered a part of the disclosure of the accompanying continuation or divisional application and is hereby incorporated by reference. The incorporation can only be relied upon when a portion has been inadvertently omitted from the submitted application parts.

18. CORRESPONDENCE ADDRESS

☐ Customer Number or Bar Code Label (Insert Customer No. or attach bar code label here) or ☒ Correspondence address below

NAME	STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.				
ADDRESS	Attorneys at Law				
ADDRESS	Suite 600, 1100 New York Avenue, N.W.				
CITY	Washington	STATE	DC	ZIP CODE	20005-3934
COUNTRY	USA	TELEPHONE	(202) 371-2600	FAX	(202) 371-2540

NAME (Print/Type)	Brian J. Del Buono	Registration No. (Attorney/Agent)	42,473
SIGNATURE		Date	October 27, 2000

Burden Hour Statement: This form is estimated to take 0.2 hours to complete. Time will vary depending upon the needs of the individual case. Any comments on the amount of time you are required to complete this form should be sent to the Chief Information Officer, U.S. Patent and Trademark Office, Washington, DC 20231. DO NOT SEND FEES OR COMPLETED FORMS TO THIS ADDRESS. SEND TO: Assistant Commissioner for Patents, Box Patent Application, Washington, DC 20231.

**FEE TRANSMITTAL
for FY 2001**

Patent fees are subject to annual revision.

Complete if Known

Application Number	To be assigned
Filing Date	HEREWITH (Oct. 27, 2001)
First Named Inventor	FOX et al.
Examiner Name	To be assigned
Group Art Unit	To be assigned
Attorney Docket No.	0942.4460002/RWE/BJD

TOTAL AMOUNT OF PAYMENT (\$710.00)

METHOD OF PAYMENT (check one)

1. ☐ The Commissioner is hereby authorized to charge indicated fees and credit any overpayment to:

Deposit Account Number 19-0036
Deposit Account Name Sterne, Kessler, Goldstein & Fox P.L.L.C.

- ☐ Charge Any Additional Fee Required Under 37 CFR §§ 1.16 and 1.17

- ☐ Applicant claims small entity status See 37 CFR 1.27

FEE CALCULATION (continued)**3. ADDITIONAL FEES**

Large Entity Small Entity

Fee Code	Fee (\$)	Fee Code	Fee (\$)	Fee Description	Fee paid
105	130	205	65	Surcharge - late filing fee or oath	
127	50	227	25	Surcharge - late provisional filing fee or cover sheet	
139	130	139	130	Non-English specification	
147	2,520	147	2,520	For filing a request for <i>ex parte</i> reexamination	
112	920*	112	920*	Requesting publication of SIR prior to Examiner action	
113	1,840*	113	1,840*	Requesting publication of SIR after Examiner action	
115	110	215	55	Extension for reply within first month	
116	390	216	195	Extension for reply within second month	
117	890	217	445	Extension for reply within third month	
118	1,390	218	695	Extension for reply within fourth month	
128	1,890	228	945	Extension for reply within fifth month	
119	310	219	155	Notice of Appeal	
120	310	220	155	Filing a brief in support of an appeal	
121	270	221	135	Request for oral hearing	
138	1,510	138	1,510	Petition to institute a public use proceeding	
140	110	240	55	Petition to revive - unavoidable	
141	1,240	241	620	Petition to revive - unintentional	
142	1,240	242	620	Utility issue fee (or reissue)	
143	440	243	220	Design issue fee	
144	600	244	300	Plant issue fee	
122	130	122	130	Petitions to the Commissioner	
123	50	123	50	Petitions related to provisional applications	
126	240	126	240	Submission of Information Disclosure Stmt	
581	40	481	40	Recording each patent assignment per property (times number of properties)	
146	710	246	355	Filing a submission after final rejection (37 CFR 1.129(a))	
149	710	249	355	For each additional invention to be examined (37 CFR 1.129(b))	
179	710	279	355	Request for Continued Examination (RCE)	
169	900	169	900	Request for expedited examination of a design application	

Other fee (specify):

Other fee (specify):

*Reduced by Basic Filing Fee Paid

SUBTOTAL (3) (\$)

FEE CALCULATION**1. BASIC FILING FEE**

Large Fee Code	Entity Fee Code	Small Fee Code	Entity Fee Code	Fee Description	Fee Paid
101	710	201	355	Utility filing fee	710.00
106	320	206	160	Design filing fee	
107	490	207	245	Plant filing fee	
108	710	208	355	Reissue filing fee	
114	150	214	75	Provisional filing fee	

SUBTOTAL (1) (\$) 710.00

2. EXTRA CLAIM FEES

Large Fee Code	Entity Fee Code	Small Fee Code	Entity Fee Code	Fee Description	Fee Paid
Total Claims	15	- 20** = 0	X 0 =		00.00
Indep. Claims	2	- 3** = 0	X 0 =		00.00
Multiple Dependent					00.00

Large Fee Code	Entity Fee Code	Small Fee Code	Entity Fee Code	Fee Description	Fee Paid
103	18	203	9	Claims in excess of 20	
102	80	202	40	Independent claims in excess of 3	
104	270	204	135	Multiple dependent claim	
108	80	208	40	*Reissue independent claims over original Patent	
110	18	210	9	*Reissue claims in excess of 20 and over original patent	

SUBTOTAL (2) (\$) 00.00

** or number previously paid, if greater. For Reissues, see above

SUBMITTED BY

Name (Print/Type) Brian J. Del Buono

Signature

Registration No.

42,473

Complete (if applicable)

Telephone 202-371-2600

Date October 27, 2000

WARNING: Information on this form may become public. Credit card information should not be included on this form. Provide credit card information and authorization on PTO-2038.

Burden Hour Statement: This form is estimated to take 0.2 hours to complete. Time will vary depending upon the needs of the individual case. Any comments on the amount of time you are required to complete this form should be sent to the Chief Information Officer, Patent and Trademark Office, Washington, DC 20231. DO NOT SEND FEES OR COMPLETED FORMS TO THIS ADDRESS. SEND TO: Assistant Commissioner for Patents, Washington, DC 20231.

S&C Rev. 10/20/00 mma

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:

FOX *et al.*

Appl. No.: (To be assigned; Divisional of U.S.
Appl. No. 09/134,672)

Filed: Herewith (October 27, 2000)

For: **Methods and Compositions for
Cloning Nucleic Acid Molecules**

Art Unit: (To be assigned)

Examiner: (To be assigned)

Atty Docket: 0942.4460002/RWE/BJD

Preliminary Amendment

Assistant Commissioner for Patents
Washington, DC 20231

Sir:

In advance of prosecution of the above-captioned divisional application, please amend the application as follows.

Amendments

Please amend the application as follows:

In the Specification:

In the specification at page 1, line 4, after "This application" please insert -- is a divisional of U.S. Application No. 09/134,672, filed August 14, 1998 (and now U.S. Patent No. 6,140,086), which --.

In the specification at page 10, line 10, please delete "VENT™" and insert therefor -- VENT® *Tli* --; and line 11, after "DEEPVENT™" please insert -- *Pyrococcus* species GB-D --.

In the specification at page 26, line 3, please delete "VENT™" and insert therefor -- VENT® --; and line 4, after "DEEPVENT™" please insert -- *Pyrococcus* species GB-D --.

In the specification at page 28, line 30, please delete "VENT™" and insert therefor -- VENT® *Tli* --.

In the specification at page 29, line 1, after "DEEPVENT™" please insert -- *Pyrococcus* species GB-D --; line 15, after "DEEPVENT™" please insert -- *Pyrococcus* species GB-D DNA polymerase --; and line 16, please delete "*Tli*/VENT™" and insert therefor -- *Tli*/VENT® --.

In the Claims:

Please cancel claims 1-36 and 44, without prejudice to or disclaimer of the subject matter contained therein.

Remarks

No new matter has been added by the foregoing amendments. The specification has been amended to update the priority information for the present divisional application, and to recite the generic terminology for the trademarks VENT® and DEEPVENT™ where appropriate in accordance with MPEP § 608.01(v). The generic terminology for VENT® DNA polymerase (*i.e.*, *Tli* DNA polymerase) is disclosed in the present specification, for example at page 26, line 3

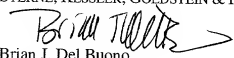
and at page 29, line 16. The generic terminology for DEEPVENT™ DNA polymerase (*i.e.*, *Pyrococcus* species GB-D DNA polymerase) is disclosed in at col. 4, lines 54-56, of U.S. Patent No. 5,512,462 (Doc. No. AE1 made of record in the parent of the present application, U.S. Application No. 09/134,672), which was incorporated by reference into the present specification (*see* specification at page 29, lines 2-3, and at page 53, lines 22-26). Hence, these amendments to the specification do not add new matter, and their entry into the application is respectfully requested. Upon entry of the foregoing amendments, claims 37-43 and 45-52 are pending in the application, with claims 37 and 45 being the independent claims.

It is not believed that extensions of time are required, beyond those that are otherwise provided for in the accompanying documents. However, if additional extensions of time are necessary to prevent abandonment of this application, then such extensions of time are hereby petitioned under 37 C.F.R. § 1.136(a), and any fees required therefor are hereby authorized to be charged to our Deposit Account No. 19-0036.

It is respectfully believed that this application is now in condition for examination. Early notice to this effect is respectfully requested.

Respectfully submitted,

STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.


Brian J. Del Buono
Agent for Applicants
Registration No. 42,473

Date: Oct. 27, 2000
1100 New York Avenue, N.W.
Suite 600
Washington, D.C. 20005-3934
(202) 371-2600
P99-05.wpd

Methods and Compositions for Cloning Nucleic Acid Molecules

CROSS REFERENCE TO RELATED APPLICATION

5 This application claims the benefit of U.S. Provisional Application No. 60/055,849, filed August 15, 1997, the disclosure of which is entirely incorporated herein by reference.

BACKGROUND OF THE INVENTION

Field of the Invention

10 This invention is in the fields of molecular and cellular biology. The invention is generally directed to amplification of nucleic acid molecules and to methods for cloning nucleic acid molecules (DNA or RNA) that have been amplified or synthesized, particularly those nucleic acid molecules that have undergone PCR amplification. In particular, the invention concerns methods of cloning amplified nucleic acid molecules comprising the use of inhibitors of nucleic acid polymerases that carry out the amplification. The invention further concerns 15 nucleic acid molecules produced by such methods and vectors and host cells comprising such nucleic acid molecules. The invention further relates to compositions for facilitating cloning of amplified nucleic acid molecules.

Related Art

20 *Cloning of Nucleic Acid Molecules*

In examining the structure and physiology of an organism, tissue or cell, it is often desirable to determine its genetic content. The genetic framework of an organism is encoded in the double-stranded sequence of nucleotide bases in the deoxyribonucleic acid (DNA) which is contained in the somatic and germ cells of 25 the organism. The genetic content of a particular segment of DNA, or gene, is only manifested upon production of the protein which the gene encodes. In order

to produce a protein, a complementary copy of one strand of the DNA double helix (the "coding" strand) is produced by polymerase enzymes, resulting in a specific sequence of ribonucleic acid (RNA). This particular type of RNA, since it contains the genetic message from the DNA for production of a protein, is called messenger RNA (mRNA).

Within a given cell, tissue or organism, there exist myriad mRNA species, each encoding a separate and specific protein. This fact provides a powerful tool to investigators interested in studying genetic expression in a tissue or cell -- mRNA molecules may be isolated and further manipulated by various molecular biological techniques, thereby allowing the elucidation of the full functional genetic content of a cell, tissue or organism.

One common approach to the study of gene expression is the production of complementary DNA (cDNA) clones. In this technique, the mRNA molecules from an organism are isolated from an extract of the cells or tissues of the organism. This isolation often employs solid chromatography matrices, such as cellulose or agarose, to which oligomers of thymidine (T) have been complexed. Since the 3' termini on most eukaryotic mRNA molecules contain a string of adenosine (A) bases, and since A binds to T, the mRNA molecules can be rapidly purified from other molecules and substances in the tissue or cell extract. From these purified mRNA molecules, cDNA copies may be made using one or more polypeptides having reverse transcriptase (RT) activity, which results in the production of single-stranded cDNA molecules. The single-stranded cDNAs may then be converted into a complete double-stranded DNA copy (*i.e.*, a double-stranded cDNA) of the original mRNA (and thus of the original double-stranded DNA sequence, encoding this mRNA, contained in the genome of the organism) by the action of a polypeptide having nucleic acid polymerase activity, such as a DNA polymerase. The protein-specific double-stranded cDNAs can then be inserted into a plasmid or viral vector (also called cloning vehicles), using controlled restriction enzyme digestion and ligation of the cDNA and the vehicle. The resulting cDNA-vehicle construct is then introduced into a bacterial host,

yeast, animal or plant cell and the host cells are then grown in culture media, resulting in a population of host cells containing (or in some cases, expressing) the gene of interest.

This entire process, from isolation of mRNA to insertion of the cDNA into a plasmid or vector to growth of host cell populations containing the isolated gene, is termed "cDNA cloning." If cDNAs are prepared from a number of different mRNAs, the resulting set of cDNAs is called a "cDNA library" which represents a population of genes comprising the functional genetic information present in the source cell, tissue or organism.

A variety of procedures are useful to clone genes. One such method entails analyzing a library of cDNA inserts (derived from a cell expressing the corresponding protein) for the presence of an insert which contains the desired gene. Such an analysis may be conducted by transfecting cells with the vector, inducing the expression of the protein, and then assaying for protein expression, for example, by immunoreaction with an antibody which is specific for the desired protein.

Alternatively, in order to detect the presence of the desired gene, one may employ an oligonucleotide (or set of oligonucleotides) which have a nucleotide sequence that is complementary to the oligonucleotide sequence or set of sequences that codes for the desired protein. Such oligonucleotides are used to detect and/or isolate the desired gene by selective hybridization. Techniques of nucleic acid hybridization are disclosed by Maniatis, T., *et al.*, In: *Molecular Cloning, a Laboratory Manual*, Cold Spring Harbor, NY (1982), and by Haymes, B.D., *et al.*, In: *Nucleic Acid Hybridization, a Practical Approach*, IRL Press, Washington, DC (1985), which references are herein incorporated by reference.

In addition to the above methods, most commonly used cloning vectors have an indicator gene which results in the expression of a specific phenotype in host cells containing the vector (e.g., blue colonies for host cells containing vectors that carry *lacZ α* ; see Maniatis, T., *et al.*, *Id.*). Insertion of heterologous nucleic acid sequences into multiple cloning sites in such vectors interrupts or

inactivates the indicator gene, resulting in non-expression of the phenotype (e.g., white colonies for the above-described host cells containing *lacZα* vectors). Such an approach provides a convenient means for differentiating recombinant clones (i.e., those forming white colonies) from non-recombinant clones (i.e., those forming blue colonies). However, this approach does not prevent the growth of non-recombinant clones.

Nucleic Acid Amplification

Soon after their identification and characterization, it was recognized that the activities of the various enzymes and cofactors involved in nucleic acid synthesis could be exploited *in vitro* to dramatically increase the concentration of, or "amplify," one or more selected nucleotide sequences. For many medical, diagnostic and forensic applications, amplification of a particular nucleic acid molecule is essential to allow its detection in, or isolation from, a sample in which it is present in very low amounts. More recently, *in vitro* amplification of specific genes has provided powerful and less costly means to facilitate the production of therapeutic proteins by molecular biological techniques, and may have applications in genetic therapy as well.

While a variety of nucleic acid amplification processes have been described, the most commonly employed is the Polymerase Chain Reaction (PCR) technique disclosed in U.S. Patent Nos. 4,683,195 and 4,683,202. In this process, a sample containing the nucleic acid sequence to be amplified (the "target sequence") is first heated to denature or separate the two strands of the nucleic acid. The sample is then cooled and mixed with specific oligonucleotide primers which hybridize to the target sequence. Following this hybridization, a buffered aqueous solution containing at least one polypeptide having DNA polymerase activity is added to the sample, along with a mixture of the dNTPs that are linked by the polymerase to the replicating nucleic acid strand. After allowing polymerization to proceed to completion, the products are again heat-denatured, subjected to another round of primer hybridization and polymerase replication, and

this process is repeated any number of times. Since each nucleic acid product of a given cycle of this process serves as a template for production of two new nucleic acid molecules (one from each parent strand), the PCR process results in an exponential increase in the concentration of the target sequence. Thus, in a well-controlled, high-fidelity PCR process, as few as 20 cycles can result in an over one million-fold amplification of the target nucleic acid sequence (See U.S. Patent Nos. 4,683,195 and 4,683,202).

Other techniques for amplification of target nucleic acid sequences have also been developed. For example, Walker *et al.* (U.S. Pat. No. 5,455,166; EP 0 684 315) described a method called Strand Displacement Amplification (SDA), which differs from PCR in that it operates at a single temperature and uses a polymerase/endonuclease combination of enzymes to generate single-stranded fragments of the target DNA sequence, which then serve as templates for the production of complementary DNA (cDNA) strands. An alternative amplification procedure, termed Nucleic Acid Sequence-Based Amplification (NASBA) was disclosed by Davey *et al.* (U.S. Pat. No. 5,409,818; EP 0 329 822). Similar to SDA, NASBA employs an isothermal reaction, but is based on the use of RNA primers for amplification rather than DNA primers as in PCR or SDA.

Amplification-Based Cloning

Standard cloning techniques such as those described above are often useful for cloning nucleic acid sequences that are expressed at relatively high levels in the source cells or tissues. However, these techniques frequently are not particularly sensitive when the starting samples contain only low levels of the nucleic acid molecule of interest. This problem is particularly important when the tissue or cell samples are themselves present in low quantities (as in many medical or forensic applications), or when the specific nucleotide sequence is present or expressed at low levels in the cell/tissue samples.

Amplification-based cloning of nucleic acid molecules, particularly that employing PCR, has been used in the attempt to overcome the lack of sensitivity

of earlier approaches (*see, e.g., Lee, C.C., et al., Science 239:1288-1291 (1988)*). There are a number of methods available for performing such cloning.

In one such method, restriction enzyme sites can be incorporated into the PCR primers; the PCR-generated nucleic acid molecules will thus contain these restriction sites. For cloning of these specific sequences, these amplified nucleic acid molecules can then be digested with restriction enzymes, the digested fragments ligated into an appropriate site within a plasmid vector, and the vector incorporated into a host cell.

Alternatively, PCR products generated by *Taq* DNA polymerase, which typically contain an additional deoxyadenosine (dA) residue at their 3' termini, can be cloned into specific cloning vectors containing 3' deoxythymidine (dT) overhangs which provide a specific recognition sequence for the 3' A residue on the PCR product. This process, often referred to as "TA cloning," provides a means of directly cloning PCR-amplified nucleic acid molecules without the need for preparation of primers with specific restriction sites (*see U.S. Patent No. 5,487,993, which is incorporated herein by reference in its entirety*).

In other cloning methods, blunt-end PCR fragments generated by cleavage with certain restriction enzymes (*e.g., SmaI, SspI or ScaI*) can be cloned into blunt-end insertion sites of cloning vectors (*see, e.g., Ausubel, F.M., et al., eds., "Current Protocols in Molecular Biology," New York: John Wiley & Sons, Inc., pp. 3.16.1-3.16.11 (1995)*), or PCR-amplified nucleic acid molecules can be cloned using uracil DNA glycosylase (UDG; *see U.S. Patent No. 5,137,814, which is incorporated herein by reference in its entirety*). Such blunt-end cloning may also be facilitated by treatment of *Taq*-amplified PCR products, which contain dA overhangs as described above, with T4 DNA polymerase to remove the dA overhangs (a procedure often termed "polishing") followed by insertion of the resulting blunt-end fragments into blunt-end vector insertion sites as generally described above.

However, the cloning of amplified nucleic acid molecules, especially by restriction enzyme digestion and insertion into cloning vehicles, is usually not

simple and straightforward. Problems that plague the investigator are low cloning efficiencies (*i.e.*, a low number of recombinant clones obtained per transformation) and cloning artifacts (*i.e.*, recombinant clones which contain a modified insert). The probable cause of such technical limitations is residual polymerase activity which remains in the reaction mixture after the amplification process (*see* Bennet, B.L., and Molenaar, A.J., *BioTechniques* 16:36-37 (1994)). In fact, it has been shown that after 30 rounds of amplification under standard PCR conditions, sufficient residual polymerase activity is present in the reaction mixture to conduct an additional 30 rounds of amplification. Upon digestion of the termini of the amplified nucleic acid molecules with restriction endonucleases to generate 3' recessed ("sticky") ends in the initial stages of cloning, this residual polymerase can utilize remaining dNTPs in the sample to fill in the 3' ends to regenerate an undesirable blunt end. This interference results in poor ligation of the digested insert into a prepared recipient cloning vector which has been manipulated to possess recessed ends compatible with those of the insert. In fact, even the addition of a single nucleotide to the 3' sticky end can inhibit the ligation process and increase the number of incorrect recombinants that an operator must screen. An additional complication is that if the insert is to be ligated into an expression vector for transformation into a host cell to ultimately generate a protein encoded by the insert, the addition of nucleotides to the digested amplification products can often shift the reading frame of the insert and result in expression of an incomplete, mutant and/or nonfunctional protein, especially if the promoter resides in the cloning vector 5' to the insert.

One often-used approach to attempting to solve this technical problem involves multiple organic phenol/chloroform extractions of the amplified nucleic acid molecules, prior to cloning, to aid in the removal of the residual polymerases. Analogous methods involve similar time-consuming technical manipulations such as successive rounds of ethanol precipitation and agarose gel purification. While such techniques may reduce the content of the amplifying polymerase to some extent, they also usually result in reduced yields of clonable product due to loss,

destruction and/or structural alteration of the amplified nucleic acid molecules during purification. Thus, the temporal and economic constraints to efficient and high-yield cloning of amplified nucleic acid molecules have yet to be overcome.

BRIEF SUMMARY OF THE INVENTION

5 The present invention relates generally to methods that overcome these temporal and economic constraints, providing for high-efficiency and rapid cloning of nucleic acid molecules, in particular amplified nucleic acid molecules. Specifically, the methods of the invention entail the use of one or more inhibitors of polymerases in the cloning procedure, whereby residual polymerase activity
10 remaining in the reaction mixture after nucleic acid synthesis or amplification is inactivated or inhibited, such that the nucleic acid molecules may be efficiently ligated into a cloning vector.

 In one embodiment, the cloning methods of the invention comprise
15 (a) amplifying or synthesizing one more nucleic acid molecules in the presence of one of more polypeptides having polymerase activity to produce copies of the nucleic acid molecules; and (b) incubating the amplified or synthesized nucleic acid molecules with one or more inhibitors of the polypeptides having polymerase activity under conditions sufficient to inhibit or inactivate the polymerase activity. These methods of the invention may further comprise digesting the amplified or
20 synthesized nucleic acid molecules with one or more restriction endonucleases, to produce digested nucleic acid molecules, ligating the amplified, synthesized or digested nucleic acid molecules into one or more vectors to form one or more genetic constructs, and transforming the genetic constructs into one or more host cells. Preferably, the inhibition or inactivation of the polypeptides having
25 polymerase activity increases the efficiency of cloning of the amplified, synthesized or digested nucleic acid molecules into one or more vectors. In addition, the inhibitors used in these methods preferably prevent or inhibit modification of one or more termini of the amplified or digested nucleic acid molecules, and allow

increased efficiency of cloning of the amplified, synthesized or digested nucleic acid molecules into one or more vectors.

The invention also relates to nucleic acid molecules produced by the above-described methods.

5 According to the invention, the amplification step of the above-described methods may comprise:

(a) contacting a first nucleic acid molecule, a first primer nucleic acid molecule which is complementary to a portion of the first nucleic acid molecule, a second nucleic acid molecule and a second primer nucleic acid molecule which is complementary to a portion of the second nucleic acid molecule, with one or more polypeptides having polymerase activity;

(b) incubating the molecules under conditions sufficient to form a third nucleic acid molecule complementary to all or a portion of the first nucleic acid molecule and a fourth nucleic acid molecule complementary to all or a portion of the second nucleic acid molecule;

(c) denaturing the first and third and the second and fourth nucleic acid molecules; and

(d) repeating steps (a) through (c) one or more times.

In another aspect, the invention relates to such methods wherein the first and/or second primer nucleic acid molecules comprise one or more recombination sites (recombinase recognition sites) or portions thereof. Nucleic acid molecules synthesized according to this aspect of the invention thus will comprise one or more recombination sites or portions thereof, thereby facilitating easy movement or exchange of nucleic acid segments between different synthesized nucleic acid molecules using one or more recombinase proteins, as described below.

In accordance with the invention, the nucleic acid synthesis step in the above methods may comprise:

(a) mixing a nucleic acid template (e.g., and RNA or a DNA molecule, preferably an mRNA molecule) with one or more polypeptides having polymerase activity; and

(b) incubating the mixture under conditions sufficient to make a nucleic acid molecule complementary to all or a portion of the template.

In preferred such aspects, the one or more DNA molecules synthesized by the above methods may be one or more double-stranded cDNA molecules.

5 The polypeptides having polymerase activity that are preferred for use in these methods of the invention may be DNA polymerases (including thermostable DNA polymerases) or reverse transcriptases. Preferred DNA polymerases include *Taq* DNA polymerase, *Tne* DNA polymerase, *Tma* DNA polymerase, *Pfu* DNA polymerase, *Tfi* DNA polymerase, *Tth* DNA polymerase, *Pwo* DNA polymerase, *Bst* DNA polymerase, *Bca* DNA polymerase, VENT™ DNA polymerase, DEEPVENT™ DNA polymerase, T7 DNA polymerase, DNA polymerase III, Klenow fragment DNA polymerase, Stoffel fragment DNA polymerase, and mutants, fragments or derivatives thereof. Preferred reverse transcriptases include M-MLV reverse transcriptase, RSV reverse transcriptase, AMV reverse transcriptase, RAV reverse transcriptase, MAV reverse transcriptase, HIV reverse transcriptase, M-MLV H⁻ reverse transcriptase, RSV H⁻ reverse transcriptase, AMV H⁻ reverse transcriptase, RAV H⁻ reverse transcriptase, MAV H⁻ reverse transcriptase and HIV H⁻ reverse transcriptase, and mutants, fragments or derivatives thereof.

20 Preferred polymerase inhibitors for use in the methods of the present invention include, but are not limited to, antibodies (particularly anti-*Taq*, anti-*Tne*, anti-*Pfu* or anti-*Tma* antibodies) or fragments thereof, chemical compounds, antibiotics, heavy metals, acids, metal chelators, nucleotide analogues, sulfhydryl reagents, anionic detergents, polyanions, captan ((N-[trichloromethyl]-thio)-4-cyclohexene-1,2-dicarboximide), acidic polysaccharides, and combinations thereof.

25 In another aspect, the invention relates to methods of ligating an amplified, synthesized or digested nucleic acid molecule into a vector with increased efficiency, comprising:

(a) forming a mixture comprising the nucleic acid molecule and one or more polymerase inhibitors; and

(b) ligating the nucleic acid molecule into one or more vectors to form one or more genetic constructs.

5 The mixtures used in these methods may optionally further comprise one or more polypeptides having polymerase activity. In addition, these methods of the invention may further comprise transforming the one or more genetic constructs into one or more host cells.

10 The invention also relates to methods for cloning one or more nucleic acid molecules into one or more vectors, comprising:

(a) forming a mixture comprising the nucleic acid molecules to be cloned (which may be amplified, synthesized or digested nucleic acid molecules), the vectors and one or more polymerase inhibitors; and

15 (b) ligating the nucleic acid molecules into the vectors to form one or more genetic constructs.

In another embodiment, the invention relates to such cloning methods wherein the one or more nucleic acid molecules and/or one or more vectors may comprise one or more engineered recombination sites.

20 In preferred such methods, the nucleic acid molecules are cDNA molecules.

These methods of the invention may further comprise transforming the one or more genetic constructs into one or more host cells.

In another embodiment, the invention relates to methods for cloning one or more nucleic acid molecules into one or more vectors, comprising:

25 (a) forming a mixture comprising the nucleic acid molecules to be cloned (which may be synthesized or amplified nucleic acid molecules), one or more polymerase inhibitors and one or more restriction endonucleases; and

(b) ligating the nucleic acid molecules into one or more vectors to form one or more genetic constructs.

In another embodiment, the invention relates to such cloning methods wherein the one or more nucleic acid molecules and/or one or more vectors may comprise one or more engineered recombination sites.

The mixtures used in these methods may optionally further comprise one or more polypeptides having polymerase activity. In addition, these methods of the invention may further comprise transforming the one or more genetic constructs into one or more host cells. In one preferred such method, the polymerase inhibitors and the restriction endonucleases may be added simultaneously. In another preferred method, the polymerase inhibitors and the restriction endonucleases may be added sequentially.

Methods of the invention may involve any standard cloning methods in which a nucleic acid molecule is inserted into a vector. In particular, the invention concerns the use of topoisomerase, which can cleave a vector to produce 3' dT overhangs and ligate an amplified fragment which contains 3' dA overhangs (produced, for example, by *Taq* DNA polymerase). Other enzymes for cleaving and ligating (*e.g.*, DNA-modifying enzymes), used in cloning nucleic acid molecules into vectors, may also be used in accordance with the invention. In the above-described methods wherein the amplification primers and/or cloned nucleic acid molecules contain one or more engineered recombination sites, for example, one or more recombination proteins may be used in the above-noted standard cloning methods. Recombination proteins which may be used in accordance with this aspect of the invention include but are not limited to site-specific recombinases, such as (a) the integrase family of recombinases (Argos *et al.* *EMBO J.* 5:433-440 (1986)) including bacteriophage λ integrase, (Landy, A. (1993) *Current Opinions in Genetics and Devel.* 3:699-707), Cre from bacteriophage P1 (Hoess and Abremski (1990) In *Nucleic Acids and Molecular Biology*, vol. 4. Eds.: Eckstein and Lilley, Berlin-Heidelberg: Springer-Verlag; pp. 90-109), and FLP from *Saccharomyces cerevisiae* (Broach *et al.*, *Cell* 29:227-234 (1982)); and (b) the resolvase family of recombinases (*e.g.*, $\gamma\delta$, Tn3 resolvase, Hin, Gin, and Cin) (Maeser and Kahnmann (1991) *Mol. Gen.*

Genet. 230:170-176). Other site-specific recombinases may also be used in accordance with the methods of the invention, including the site-specific recombination proteins encoded by bacteriophage lambda, phi 80, P22, P2, 186, P4 and P1 which are known in the art.

5 In another aspect, the invention also relates to kits for cloning an amplified, synthesized or digested nucleic acid molecule. Kits according to the invention may comprise one or more containers containing one or more of the above-described polymerase inhibitors. Such kits may further comprise one or more additional containers containing, for example, one or more polypeptides having
10 polymerase activity, one or more primer nucleic acid molecules, one or more nucleotides, one or more polypeptides having reverse transcriptase activity, one or more ligases, one or more vectors, one or more host cells (which may be competent for transformation), one or more topoisomerases and one or more restriction endonucleases.

15 The invention also relates to compositions comprising one or more restriction endonucleases and one or more of the above-described polymerase inhibitors, either or both of which may be stable upon storage. Compositions of the invention also comprise the above-described polymerase inhibitors and one or more DNA modifying enzymes or combinations thereof (such as ligases, kinases, phosphatases, nucleases, endonucleases, topoisomerases, gyrases, terminal
20 deoxynucleotidyl transferases, etc.) Compositions according to this aspect of the invention may further comprise one or more additional components, including, for example, one or more nucleic acid molecules or one or more suitable buffers.

25 Other preferred embodiments of the present invention will be apparent to one of ordinary skill in light of the following drawings and description of the invention, and of the claims.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 is an autoradiograph of a 552 bp amplification product obtained by *Taq* polymerase-mediated amplification of a 664 bp amplicon of the 3' end of the chloramphenicol acetyltransferase (CAT) gene. Following amplification, the 552 bp product was incubated in the presence or absence of two different preparations of anti-*Taq* antibodies prior to being digested with *Eco*RI and *Hind*III in the presence of ³²P-dATP, and samples were then resolved on a 1% TBE-agarose gel followed by autoradiography. Lanes 1, 2, 6 and 7: no antibody treatment; lanes 3, 4 and 5: antibody preparation #1, at 1 unit, 0.67 unit and 0.33 unit, respectively; lanes 8, 9 and 10: antibody preparation #2, at 1 unit, 0.67 unit and 0.33 unit, respectively; lane 11: restriction enzyme digestion followed by treatment of samples with Klenow fragment (positive control).

DETAILED DESCRIPTION OF THE INVENTION

Definitions

In the description that follows, a number of terms conventionally used in the fields of molecular biology and protein engineering, and therefore generally understood by those of routine skill in the art, are utilized extensively. Certain terms as used herein, however, have specific meanings for the purposes of the present invention. In order to provide a clear and consistent understanding of the specification and claims, and the scope to be given such terms, the following definitions are provided.

The term "polypeptide" is used herein to mean a sequence of contiguous amino acids, of any length. As used herein, the terms "peptide" or "protein" may be used interchangeably with the term "polypeptide."

As used herein, "nucleotide" refers to a base-sugar-phosphate combination. Nucleotides are monomeric units of a nucleic acid sequence (DNA and RNA).

The term nucleotide includes deoxyribonucleoside triphosphates ("dNTPs") such as dATP, dCTP, dITP, dUTP, dGTP, dTTP, or derivatives thereof. Such derivatives include, for example, [α S]dATP, 7-deaza-dGTP and 7-deaza-dATP. The term nucleotide as used herein also refers to dideoxyribonucleoside triphosphates ("ddNTPs") and their derivatives, including, but not limited to, ddATP, ddCTP, ddGTP, ddITP, and ddTTP. In addition, the term nucleotide includes ribonucleoside triphosphates (rNTPs) such as rATP, rCTP, rITP, rUTP, rGTP, rTTP and their derivatives, which are analogous to the above-described dNTPs and ddNTPs except that the rNTPs comprise ribose instead of deoxyribose or dideoxyribose in their sugar-phosphate backbone. According to the present invention, a "nucleotide" may be unlabeled or detectably labeled by well known techniques. Detectable labels include, for example, radioactive isotopes, fluorescent labels, chemiluminescent labels, bioluminescent labels and enzyme labels.

The term "nucleic acid molecule" as used herein refers to a sequence of contiguous nucleotides (dNTPs or ddNTPs, or combinations thereof) which may encode a full-length polypeptide or a fragment of any length thereof, or which may be non-coding.

The term "dNTP" (plural "dNTPs") generically refers to the deoxynucleoside triphosphates (*e.g.*, dATP, dCTP, dGTP, dTTP, dUTP, dITP, 7-deaza-dGTP, α dATP, α dTTP, α dGTP and α dCTP), and the term "ddNTP" (plural "ddNTPs") to their dideoxy counterparts, that are incorporated by polymerase enzymes into newly synthesized nucleic acids.

The term "unit" as used herein refers to the activity of an enzyme. When referring to a DNA polymerase, one unit of activity is the amount of enzyme that will incorporate 10 nanomoles of dNTPs into acid-insoluble material (*i.e.*, DNA or RNA) in 30 minutes under standard primed DNA synthesis conditions.

The terms "stable" and "stability" as used herein generally mean the retention by an enzyme of at least 70%, preferably at least 80%, and most preferably at least 90%, of the original enzymatic activity (in units) after the

enzyme or composition containing the enzyme has been stored for at least four weeks at a temperature of about 20-25°C, at least one year at a temperature of about 4°C or at least 2 years at a temperature of -20°C.

As used herein, a "cloning vector" or "cloning vehicle" is a plasmid, cosmid or phage DNA or other DNA molecule which is able to replicate autonomously in a host cell, and which is characterized by one or a small number of restriction endonuclease recognition sites at which such DNA sequences may be cut in a determinable fashion without loss of an essential biological function of the vector, and into which DNA may be spliced in order to bring about its replication and cloning. The cloning vector or vehicle may further contain a marker suitable for use in the identification of cells transformed with the cloning vector. Markers, for example, are tetracycline resistance or ampicillin resistance.

As used herein, a "primer" refers to a single-stranded oligonucleotide that is extended by covalent bonding of nucleotide monomers during amplification or polymerization of a DNA molecule

The term "template" as used herein refers to a double-stranded or single-stranded nucleic acid molecule which is to be amplified, synthesized or sequenced. In the case of a double-stranded DNA molecule, denaturation of its strands to form a first and a second strand is performed before these molecules may be amplified, synthesized or sequenced. A primer, complementary to a portion of a DNA template is hybridized under appropriate conditions and the DNA polymerase of the invention may then synthesize a DNA molecule complementary to said template or a portion thereof. The newly synthesized DNA molecule, according to the invention, may be equal or shorter in length than the original DNA template. Mismatch incorporation or strand slippage during the synthesis or extension of the newly synthesized DNA molecule may result in one or a number of mismatched base pairs. Thus, the synthesized DNA molecule need not be exactly complementary to the DNA template.

The term "incorporating" as used herein means becoming a part of a DNA molecule or primer.

As used herein, "amplification" refers to any *in vitro* method for increasing the number of copies of a nucleotide sequence with the use of a polymerase. Nucleic acid amplification results in the incorporation of nucleotides into a nucleic acid (e.g., DNA) molecule or primer thereby forming a new nucleic acid molecule complementary to the nucleic acid template. The formed nucleic acid molecule and its template can be used as templates to synthesize additional nucleic acid molecules. As used herein, one amplification reaction may consist of many rounds of nucleic acid synthesis. Amplification reactions include, for example, polymerase chain reactions (PCR). One PCR reaction may consist of 5 to 100 "cycles" of denaturation and synthesis of a nucleic acid molecule.

An "oligonucleotide" as used herein refers to a synthetic or natural molecule comprising a covalently linked sequence of nucleotides which are joined by a phosphodiester bond between the 3' position of the pentose of one nucleotide and the 5' position of the pentose of the adjacent nucleotide.

As used herein, "thermostable" refers to an enzyme (such as a polypeptide having nucleic acid polymerase or reverse transcriptase activity) which is resistant to inactivation by heat. DNA polymerases synthesize the formation of a DNA molecule complementary to a single-stranded DNA template by extending a primer in the 5'-to-3' direction. This activity for mesophilic DNA polymerases may be inactivated by heat treatment. For example, the activities of T5 and T7 DNA polymerases are totally inactivated by exposing the enzymes to a temperature of 90°C for 30 seconds. As used herein, a thermostable DNA polymerase activity is more resistant to heat inactivation than a mesophilic DNA polymerase. However, a thermostable DNA polymerase does not mean to refer to an enzyme which is totally resistant to heat inactivation; thus heat treatment may reduce the DNA polymerase activity to some extent. A thermostable DNA polymerase typically will also have a higher optimum temperature than mesophilic DNA polymerases.

The terms "hybridization" and "hybridizing" as used herein refer to the pairing of two complementary single-stranded nucleic acid molecules (RNA and/or

DNA) to give a double-stranded molecule. As used herein, two nucleic acid molecules may be hybridized, although the base pairing is not completely complementary. Accordingly, mismatched bases do not prevent hybridization of two nucleic acid molecules provided that appropriate conditions, well known in the art, are used. In the present invention, the term "hybridization" refers particularly to hybridization of an oligonucleotide to a DNA template molecule.

"Working concentration" is used herein to mean the concentration of a reagent that is at or near the optimal concentration used in a solution to perform a particular function (such as amplification or digestion of a nucleic acid molecule). The working concentration of a reagent is also described equivalently as a "1X concentration" or a "1X solution" (if the reagent is in solution) of the reagent. Accordingly, higher concentrations of the reagent may also be described based on the working concentration; for example, a "2X concentration" or a "2X solution" of a reagent is defined as a concentration or solution that is twice as high as the working concentration of the reagent; a "5X concentration" or a "5X solution" is five times as high as the working concentration of the reagent; and so on.

The terms "recombinase" and "recombination protein" as used herein may be used interchangeably, and refer to an excisive or integrative protein, enzyme, co-factor or associated protein that is involved in recombination reactions involving one or more recombination sites, such as an enzyme which catalyzes the exchange of DNA segments at specific recombination sites. See, Landy, A., *Ann. Rev. Biochem.* 58:913-949 (1989).

The terms "recognition sequence" or "recombination site" as used herein refer to a particular DNA sequence which a protein, DNA, or RNA molecule (e.g., a restriction endonuclease, a modification methylase, or a recombinase) recognizes and binds. For example, the recognition sequence for Cre recombinase is *loxP* which is a 34 base pair sequence comprised of two 13 base pair inverted repeats (serving as the recombinase binding sites) flanking an 8 base pair core sequence. See Figure 1 of Sauer, B., *Current Opinion in Biotechnology*

5:521-527 (1994). Other examples of recognition sequences are the *attB*, *attP*, *attL*, and *attR* sequences which are recognized by the recombinase enzyme λ Integrase. *attB* is an approximately 25 base pair sequence containing two 9 base pair core-type Int binding sites and a 7 base pair overlap region. *attP* is an approximately 240 base pair sequence containing core-type Int binding sites and arm-type Int binding sites as well as sites for auxiliary proteins IHF, FIS, and Xis. See Landy, *Current Opinion in Biotechnology* 3:699-707 (1993). Such sites are also engineered according to the present invention to enhance methods and products.

10 The phrase "recombinational cloning" is used herein to mean a method whereby segments of DNA molecules are exchanged, inserted, replaced, substituted or modified, *in vitro* or *in vivo*.

15 Other terms used in the fields of recombinant DNA technology and molecular and cell biology as used herein will be generally understood by one of ordinary skill in the applicable arts.

Overview

20 The present invention is generally directed to methods that overcome the above-described temporal and economic constraints that are typically encountered during attempts to clone amplified or synthesized nucleic acid molecules. Thus, the invention provides methods that result in high-efficiency and rapid cloning of amplified, synthesized or digested nucleic acid molecules. Specifically, the methods of the invention entail the use of one or more inhibitors of nucleic acid polymerases in the cloning procedure, whereby residual polymerase activity remaining in the reaction mixture after amplification or synthesis is inactivated or inhibited. By the methods of the invention, amplified, synthesized or digested nucleic acid molecules may be quickly and efficiently ligated (using ligases, topoisomerases, etc.) into cloning vectors, and these vectors then inserted into host cells, for example for expression of the cloned nucleic acid molecules.

Methods according to this aspect of the invention may comprise one or more steps. One example is a method of cloning an amplified or synthesized nucleic acid molecule, comprising:

- 5 (a) amplifying or synthesizing one more nucleic acid molecules in the presence of one or more polypeptides having polymerase activity to produce amplified nucleic acid molecules; and
- (b) incubating the nucleic acid molecules with one or more inhibitors of the polypeptides having polymerase activity under conditions sufficient to inhibit or inactivate the polymerase activity.

10 Sources of Nucleic Acid Template Molecules

Using the methods of the invention, synthesized, amplified or digested nucleic acid molecules may be derived from a variety of sources. Nucleic acid molecules suitably cloned by the methods of the present invention may be DNA molecules (including cDNA molecules), RNA molecules (including polyadenylated

15 RNA (polyA+ RNA), messenger RNA (mRNA), transfer RNA (tRNA) and ribosomal RNA (rRNA) molecules) or DNA-RNA hybrid molecules, and may be single-stranded or double-stranded.

The nucleic acid molecules to be cloned according to the methods of the present invention may be prepared synthetically according to standard organic

20 chemical synthesis methods that will be familiar to one of ordinary skill. More preferably, the nucleic acid molecules may be obtained from natural sources, such as a variety of cells, tissues, organs or organisms. Cells that may be used as sources of nucleic acid molecules may be prokaryotic (bacterial cells, including those of species of the genera *Escherichia*, *Bacillus*, *Serratia*, *Salmonella*,

25 *Staphylococcus*, *Streptococcus*, *Clostridium*, *Chlamydia*, *Neisseria*, *Treponema*, *Mycoplasma*, *Borrelia*, *Legionella*, *Pseudomonas*, *Mycobacterium*, *Helicobacter*, *Erwinia*, *Agrobacterium*, *Rhizobium*, and *Streptomyces*) or eukaryotic (including fungi (especially yeasts), plants, protozoans and other parasites, and animals including insects (particularly *Drosophila* spp. cells), nematodes (particularly

Caenorhabditis elegans cells), and mammals (particularly human, rodent (rat or mice), monkey, ape, canine, feline, equine, bovine and ovine cells, and most particularly human cells)).

Mammalian somatic cells that may be used as sources of nucleic acids include blood cells (reticulocytes and leukocytes), endothelial cells, epithelial cells, neuronal cells (from the central or peripheral nervous systems), muscle cells (including myocytes and myoblasts from skeletal, smooth or cardiac muscle), connective tissue cells (including fibroblasts, adipocytes, chondrocytes, chondroblasts, osteocytes and osteoblasts) and other stromal cells (*e.g.*, macrophages, dendritic cells, Schwann cells). Mammalian germ cells (spermatocytes and oocytes) may also be used as sources of nucleic acids for use in the invention, as may the progenitors, precursors and stem cells that give rise to the above somatic and germ cells (*e.g.*, embryonic stem cells). Also suitable for use as nucleic acid sources are mammalian tissues or organs such as those derived from brain, kidney, liver, pancreas, blood, bone marrow, muscle, nervous, skin, genitourinary, circulatory, lymphoid, gastrointestinal and connective tissue sources, as well as those derived from a mammalian (including human) embryo or fetus.

Any of the above prokaryotic or eukaryotic cells, tissues and organs may be normal, diseased, transformed, established, progenitors, precursors, fetal or embryonic. Diseased cells may, for example, include those involved in infectious diseases (caused by bacteria, fungi or yeast, viruses (including HIV) or parasites), in genetic or biochemical pathologies (*e.g.*, cystic fibrosis, hemophilia, Alzheimer's disease, muscular dystrophy or multiple sclerosis) or in cancerous processes. Transformed or established animal cell lines may include, for example, COS cells, CHO cells, VERO cells, BHK cells, HeLa cells, HepG2 cells, K562 cells, F9 cells and the like. Other cells, cell lines, tissues, organs and organisms suitable as sources of nucleic acids for use in the present invention will be apparent to one of ordinary skill in the art.

In addition, such nucleic acid molecules and cDNA libraries may be obtained commercially, for example from Life Technologies, Inc. (Rockville, Maryland) and other commercial suppliers that will be familiar to the skilled artisan.

5 Once the starting cells, tissues, organs, libraries or other samples are obtained, nucleic acid molecules to be cloned by the methods of the invention may be isolated by methods that are well-known in the art (*See, e.g.,* Maniatis, T., *et al., Cell* 15:687-701 (1978); Okayama, H., and Berg, P., *Mol. Cell. Biol.* 2:161-170 (1982); Gubler, U., and Hoffman, B.J., *Gene* 25:263-269 (1983)). The
10 nucleic acid molecules thus isolated may then be cloned using the methods of the present invention.

Amplified Nucleic Acid Molecules

 Preferably, the nucleic acid molecules to be cloned are amplified nucleic acid molecules. Nucleic acid molecules may be amplified by a number of methods,
15 which may comprise one or more steps. For example, one such method comprises (a) contacting a first nucleic acid molecule, a first primer molecule which is complementary to a portion of the first nucleic acid molecule, a second nucleic acid molecule and a second primer molecule which is complementary to a portion of the second nucleic acid molecule, with one or more polypeptides having
20 polymerase activity; (b) incubating the molecules and one or more polypeptides under conditions sufficient to form a third nucleic acid molecule complementary to all or a portion of the first nucleic acid molecule and a fourth nucleic acid molecule complementary to all or a portion of the second nucleic acid molecule; (c) denaturing the first and third and the second and fourth nucleic acid molecules; and (d) repeating steps (a) through (c) one or more times. Such amplification
25 methods may be accomplished by any of a variety of techniques, including but not limited to use of the polymerase chain reaction (PCR; U.S. Patent Nos. 4,683,195 and 4,683,202), Strand Displacement Amplification (SDA; U.S. Patent No.

5,455,166), and Nucleic Acid Sequence-Based Amplification (NASBA; U.S. Patent No. 5,409,818); particularly preferred is PCR.

In another aspect, the invention relates to the above-described nucleic acid synthesis or amplification methods, wherein the first and/or second primer nucleic acid molecules used in the above-described amplification methods comprise one or more recombination sites (recombinase recognition sites) or portions thereof. Nucleic acid molecules synthesized or amplified according to this aspect of the invention thus will comprise one or more recombination sites or portions thereof, thereby facilitating easy movement or exchange of nucleic acid segments between different synthesized nucleic acid molecules using one or more recombinase proteins in a process termed recombinational cloning, as described below. Preferred combinations of recombination sites/recombinase proteins for use according to this aspect of the invention include the Integrase/*att* system from bacteriophage λ (Landy, A. (1993) *Current Opinions in Genetics and Devel.* 3:699-707); the Cre/*loxP* system from bacteriophage P1 (Hoess and Abremski (1990) In *Nucleic Acids and Molecular Biology*, vol. 4. Eds.: Eckstein and Lilley, Berlin-Heidelberg: Springer-Verlag; pp. 90-109); the FLP/FRT system from the *Saccharomyces cerevisiae* 2 μ circle plasmid (Broach *et al.* *Cell* 29:227-234 (1982); the resolvase family (*e.g.*, $\gamma\delta$, Tn3 resolvase, Hin, Gin, and Cin) (Maeser and Kahnmann (1991) *Mol. Gen. Genet.* 230:170-176); and site-specific recombination proteins encoded by bacteriophage lambda, phi 80, P22, P2, 186, P4 and P1. Methods for preparation of primers comprising one or more recombination sites, and use of such primers in synthesizing or amplifying one or more nucleic acid molecule products which comprise one or more recombination sites, are described in detail in commonly owned, co-pending U.S. Application Nos. 08/486,139, filed June 7, 1995; 60/065,930, filed October 24, 1997; and 09/005,476, filed January 12, 1998, the disclosures of all of which are incorporated herein by reference in their entireties.

In one embodiment of the present invention, the amplified nucleic acid fragments may be cloned (ligated) directly into one or more vectors to produce

one or more genetic constructs. The genetic constructs may then be transformed into one or more host cells.

In other cloning methods, amplified molecules cleaved or digested with one or more restriction enzymes or one or more recombination proteins as described in more detail below can be cloned into appropriate insertion sites of cloning vectors (*see, e.g.,* Ausubel, F.M., *et al.*, eds., "Current Protocols in Molecular Biology," New York: John Wiley & Sons, Inc., pp. 3.16.1-3.16.11 (1995)). Restriction enzymes used for cleavage of the amplified molecules may include blunt-end cutters (*e.g., SmaI, SspI, ScaI*, etc.) and sticky-end cutters (*e.g., HindIII, BamHI, KpnI*, etc.). Amplified nucleic acid molecules can also be cloned using uracil DNA glycosylase (UDG; *see* U.S. Patent No. 5,137,814, which is incorporated herein by reference in its entirety).

In another aspect of the invention, restriction enzyme sites can be incorporated into the amplification primers; the amplified nucleic acid molecules will thus contain these restriction sites. For cloning of these specific sequences, these amplified nucleic acid molecules can then be digested with restriction enzymes, the digested fragments ligated into an appropriate site within a plasmid vector, and the vector incorporated into a host cell as described in more detail below.

In another aspect of the invention, recombination or recombinase recognition sites can be incorporated into the amplification primers; the amplified nucleic acid molecules will thus contain these recombination or recombinase recognition sites. These amplified nucleic acid molecules can then be treated with one or more recombinations proteins as described below, to facilitate exchange or recombination of one or more nucleic acid segments between different amplified nucleic acid molecules, in a process known as recombinational cloning. The resulting recombined nucleic acid molecules may then be inserted into a plasmid vector, and the vector incorporated into a host cell as described in more detail below.

Amplified products generated by DNA polymerases which incorporate an additional deoxyadenosine (dA) residue at the 3' termini of the products (e.g., *Taq* DNA polymerase), can be cloned into specific cloning vectors containing 3' deoxythymidine (dT) overhangs which provide a specific recognition sequence for the 3' A residue on the amplified product. This process, often referred to as "TA cloning," provides a means of directly cloning amplified nucleic acid molecules without the need for preparation of primers with specific restriction sites (see U.S. Patent No. 5,487,993, which is incorporated herein by reference in its entirety). Alternatively, a ligase-independent strategy for cloning may be used (such as Topo-TA Cloning®, Invitrogen, Carlsbad, California). Blunt-end cloning of such amplified molecules containing dA overhangs may be facilitated by using T4 DNA polymerase to remove the dA overhangs (a procedure often termed "polishing") followed by insertion of the resulting blunt-end fragments into blunt-end vector insertion sites as described in more detail below.

Polymerases and Reverse Transcriptases

A variety of polypeptides having polymerase activity are useful in the methods of the present invention. Included among these polypeptides are enzymes such as nucleic acid polymerases (including DNA polymerases and RNA polymerases), as well as polypeptides having reverse transcriptase (i.e., RNA-dependent DNA polymerase) activity.

Polypeptides having reverse transcriptase activity that may be advantageously used in the present methods include, but are not limited to, Moloney Murine Leukemia Virus (M-MLV) reverse transcriptase, Rous Sarcoma Virus (RSV) reverse transcriptase, Avian Myeloblastosis Virus (AMV) reverse transcriptase, Rous-Associated Virus (RAV) reverse transcriptase, Myeloblastosis Associated Virus (MAV) reverse transcriptase, Human Immunodeficiency Virus (HIV) reverse transcriptase, retroviral reverse transcriptase, retrotransposon reverse transcriptase, hepatitis B reverse transcriptase, cauliflower mosaic virus reverse transcriptase, bacterial reverse transcriptase, *Thermus thermophilus* (*Tth*)

DNA polymerase, *Thermus aquaticus* (*Taq*) DNA polymerase, *Thermotoga neopolitana* (*Tne*) DNA polymerase, *Thermotoga maritima* (*Tma*) DNA polymerase, *Thermococcus litoralis* (*Tli* or VENT™) DNA polymerase, *Pyrococcus furiosus* (*Pfu*) DNA polymerase, DEEPVENT™ DNA polymerase, *Pyrococcus woosii* (*Pwo*) DNA polymerase, *Bacillus sterothermophilus* (*Bst*) DNA polymerase, *Bacillus caldophilus* (*Bca*) DNA polymerase, *Sulfolobus acidocaldarius* (*Sac*) DNA polymerase, *Thermoplasma acidophilum* (*Tac*) DNA polymerase, *Thermus flavus* (*Tfl/Tub*) DNA polymerase, *Thermus ruber* (*Tru*) DNA polymerase, *Thermus brockianus* (DYNAZYME™) DNA polymerase, *Methanobacterium thermoautotrophicum* (*Mth*) DNA polymerase, and mutants, variants and derivatives thereof. Particularly preferred for use in the invention are the variants of these enzymes that are substantially reduced in RNase H activity (*i.e.*, "RNase H" enzymes). By an enzyme "substantially reduced in RNase H activity" is meant that the enzyme has less than about 20%, more preferably less than about 15%, 10% or 5%, and most preferably less than about 2%, of the RNase H activity of a wildtype or "RNase H" enzyme such as wildtype M-MLV or AMV reverse transcriptases. The RNase H activity of any enzyme may be determined by a variety of assays, such as those described, for example, in U.S. Patent No. 5,244,797, in Kotewicz, M.L., *et al.*, *Nucl. Acids Res.* 16:265 (1988) and in Gerard, G.F., *et al.*, *FOCUS* 14(5):91 (1992), the disclosures of all of which are fully incorporated herein by reference. Particularly preferred RNase H⁻ reverse transcriptase enzymes for use in the invention include, but are not limited to, M-MLV H⁻ reverse transcriptase, RSV H⁻ reverse transcriptase, AMV H⁻ reverse transcriptase, RAV H⁻ reverse transcriptase, MAV H⁻ reverse transcriptase and HIV H⁻ reverse transcriptase. It will be understood by one of ordinary skill, however, that any enzyme capable of producing a DNA molecule from a ribonucleic acid molecule (*i.e.*, having reverse transcriptase activity) that is substantially reduced in RNase H activity may be equivalently used in the compositions, methods and kits of the invention.

Enzymes used in the invention may have distinct reverse transcription pause sites with respect to the template nucleic acid. Whether or not two enzymes have distinct reverse transcription pause sites may be determined by a variety of assays, including, for example, electrophoretic analysis of the chain lengths of DNA molecules produced by the two enzymes (Weaver, D.T., and DePamphilis, M.L., *J. Biol. Chem.* 257(4):2075-2086 (1982); Abbotts, J., *et al.*, *J. Biol. Chem.* 268(14):10312-10323 (1993)), or by other assays that will be familiar to one of ordinary skill in the art. As described above, these distinct transcription pause sites may represent secondary structural and sequence barriers in the nucleic acid template which occur frequently at homopolymer stretches. Thus, for example, the second enzyme may reverse transcribe to a point (e.g., a hairpin) on the template nucleic acid that is proximal or distal (i.e., 3' or 5') to the point to which the first enzyme reverse transcribes the template nucleic acid. This combination of two or more enzymes having distinct reverse transcription pause sites facilitates production of full-length cDNA molecules since the secondary structural and sequence barriers may be overcome.

Polypeptides having reverse transcriptase activity for use in the invention may be obtained commercially, for example from Life Technologies, Inc. (Rockville, Maryland), Pharmacia (Piscataway, New Jersey), Sigma (Saint Louis, Missouri) or Boehringer Mannheim Biochemicals (Indianapolis, Indiana). Alternatively, polypeptides having reverse transcriptase activity may be isolated from their natural viral or bacterial sources according to standard procedures for isolating and purifying natural proteins that are well-known to one of ordinary skill in the art (see, e.g., Houts, G.E., *et al.*, *J. Virol.* 29:517 (1979)). In addition, the polypeptides having reverse transcriptase activity may be prepared by recombinant DNA techniques that are familiar to one of ordinary skill in the art (see, e.g., Kotewicz, M.L., *et al.*, *Nucl. Acids Res.* 16:265 (1988); Soltis, D.A., and Skalka, A.M., *Proc. Natl. Acad. Sci. USA* 85:3372-3376 (1988)).

Nucleic acid polymerases such as DNA polymerases for use in the present methods may be isolated from natural or recombinant sources, by techniques that

are well-known in the art (See WO 92/06200, U.S. Patent Nos. 5,455,170 and 5,466,591, WO 96/10640 and U.S. Patent Application No. 08/370,190, filed January 9, 1995), from a variety of thermophilic bacteria that are available commercially (for example, from American Type Culture Collection, Rockville, Maryland) or may be obtained by recombinant DNA techniques (see, e.g., WO 96/10640 and U.S. Patent Application No. 08/370,190, filed January 9, 1995). Suitable for use as sources of thermostable polymerases or the genes thereof for expression in recombinant systems are the thermophilic bacteria *Thermus thermophilus*, *Thermococcus litoralis*, *Pyrococcus furiosus*, *Pyrococcus woosii* and other species of the *Pyrococcus* genus, *Bacillus stercorophilus*, *Sulfolobus acidocaldarius*, *Thermoplasma acidophilum*, *Thermus flavus*, *Thermus ruber*, *Thermus Brockianus*, *Thermotoga neapolitana*, *Thermotoga maritima* and other species of the *Thermotoga* genus, and *Methanobacterium thermoautotrophicum*, and mutants, variants or derivatives thereof. It is to be understood, however, that thermostable DNA polymerases from other organisms may also be used in the present invention without departing from the scope or preferred embodiments thereof. As an alternative to isolation, thermostable DNA polymerases are available commercially from, for example, Life Technologies, Inc. (Rockville, Maryland), New England Biolabs (Beverly, Massachusetts), Finnzymes Oy (Espoo, Finland), Stratagene (La Jolla, California), Boehringer Mannheim Biochemicals (Indianapolis, Indiana) and Perkin Elmer Cetus (Norwalk, Connecticut).

DNA polymerases used in accordance with the invention may be any enzyme that can synthesize a DNA molecule from a nucleic acid template, typically in the 5' to 3' direction. The nucleic acid polymerases used in the present invention may be mesophilic or thermophilic, and are preferably thermophilic. Preferred mesophilic DNA polymerases include T7 DNA polymerase, T5 DNA polymerase, Klenow fragment DNA polymerase, DNA polymerase III and the like. Preferred thermostable DNA polymerases that may be used in the methods of the invention include *Taq*, *Tne*, *Tma*, *Pfu*, *Tfl*, *Tth*, Stoffel fragment, VENT™

and DEEPVENT™ DNA polymerases, and mutants, variants and derivatives thereof (U.S. Patent No. 5,436,149; U.S. Patent No. 5,512,462; WO 92/06188; WO 92/06200; WO 96/10640; Barnes, W.M., *Gene* 112:29-35 (1992); Lawyer, F.C., *et al.*, *PCRMeth. Appl.* 2:275-287 (1993); Flaman, J.-M., *et al.*, *Nucl. Acids Res.* 22(15):3259-3260 (1994)). For amplification of long nucleic acid molecules (e.g., nucleic acid molecules longer than about 3-5 Kb in length), at least two DNA polymerases (one substantially lacking 3' exonuclease activity and the other having 3' exonuclease activity) are typically used. See U.S. Patent No. 5,436,149; U.S. Patent No. 5,512,462; Barnes, W.M., *Gene* 112:29-35 (1992); and co-pending U.S. Patent Application No. 08/689,815, filed February 14, 1997, the disclosures of which are incorporated herein in their entireties. Examples of DNA polymerases substantially lacking in 3' exonuclease activity include, but are not limited to, *Taq*, *The(exo)*, *Tma(exo)*, *Pfu(exo)*, *Pwo(exo)* and *Tth* DNA polymerases, and mutants, variants and derivatives thereof. Nonlimiting examples of DNA polymerases having 3' exonuclease activity include *Pfu*, DEEPVENT™, *Thi/VENT™*, *The*, *Tma*, and mutants, variants and derivatives thereof.

Polypeptides having nucleic acid polymerase and/or reverse transcriptase activity are preferably used in the present methods at a final concentration in solution of about 0.1-200 units per milliliter, about 0.1-50 units per milliliter, about 0.1-40 units per milliliter, about 0.1-36 units per milliliter, about 0.1-34 units per milliliter, about 0.1-32 units per milliliter, about 0.1-30 units per milliliter, or about 0.1-20 units per milliliter, and most preferably at a concentration of about 20 units per milliliter. Of course, other suitable concentrations of reverse transcriptase enzymes and nucleic acid polymerases suitable for use in the invention will be apparent to one of ordinary skill in the art.

Cloning of Nucleic Acid Molecules

The methods of the invention may further comprise one or more additional steps designed to facilitate the cloning of the amplified or synthesized nucleic acid molecules. For example, nucleic acid molecules amplified or synthesized as

described above may be digested with one or more restriction endonucleases, to produce a collection of digested nucleic acid molecules. Suitable methods and enzymes for use in digesting nucleic acid molecules will be familiar to one of ordinary skill in the art (see, e.g., Sambrook, J., et al., *Molecular Cloning: A Laboratory Manual*, 2nd ed., Cold Spring Harbor, New York: Cold Spring Harbor Laboratory Press (1989)). Restriction endonucleases that may be advantageously used in the methods of the invention include, but are not limited to, *Ahl*I, *Eco*47 III, *Eco*RV, *Fsp*I, *Hpa*I, *Msc*I, *Nru*I, *Pvu*II, *Rsa*I, *Sca*I, *Sma*I, *Ssp*I, *Stu*I, *Tha*I, *Ava*I, *Bam*HI, *Ban*II, *Bgl*II, *Cla*I, *Eco*RI, *Hind*III, *Hpa*II, *Kpn*I, *Mse*I, *Nco*I, *Nde*I, *Nof*I, *Pst*I, *Pvu*I, *Sac*I/*Sst*I, *Sal*I, *Xba*I, *Xho*I and I-*Ceu*I. Such restriction endonucleases are available commercially, for example from Life Technologies, Inc. (Rockville, Maryland), Sigma (St. Louis, Missouri) and New England BioLabs (Beverly, Massachusetts). Topoisomerases or other nucleic acid-modifying enzymes may also be used.

In alternative cloning methods of the invention, amplified nucleic acid molecules that comprise one or more recombination sites may be treated with one or more recombination proteins which recognize, bind to, and cleave the nucleic acid molecules at the specific recombination sites. Preferred recombination proteins for use in this aspect of the invention include those described above, such as the Int, IHF or Xis integrases; Cre; $\gamma\delta$, Tn3 resolvase, Hin, Gin, Cin, FLP; and other recombination proteins encoded by bacteriophage λ , phi 80, P22, P2, 186, P4 and P1. Appropriate methods using such recombination proteins in cloning of nucleic acid molecules comprising one or more recombination sites are described in detail in commonly owned, co-pending U.S. Application Nos. 08/486,139, filed June 7, 1995; 60/065,930, filed October 24, 1997; and 09/005,476, filed January 12, 1998, the disclosures of all of which are incorporated herein by reference in their entireties.

Once the synthesized or amplified nucleic acid molecules have been digested with one or more restriction enzymes or cleaved with one or more recombination proteins, the digested or cleaved nucleic acid molecules may be

inserted (typically by ligation, for example using a polypeptide having nucleic acid ligase activity such as T4 DNA ligase, topoisomerase or the like) into one or more vectors, such as one or more expression vectors, to yield one or more genetic constructs. Alternatively, the amplified or synthesized nucleic acid molecules may be ligated directly into one or more vectors without being digested or cleaved, to form one or more genetic constructs. Genetic constructs according to this aspect of the invention thus typically comprise the amplified, synthesized or digested/cleaved nucleic acid molecule (or fragments thereof) and the vector or cloning vehicle. These genetic constructs may, in turn, be introduced into host cells using well-known techniques such as infection, transduction, transfection, electroporation and transformation, for the large-scale production of cDNA libraries or plasmids comprising the amplified, synthesized or digested/cleaved nucleic acid molecules, or for the expression of the amplified, synthesized or digested/cleaved nucleic acid molecules. The vectors may be, for example, a phage, plasmid, viral or retroviral vector, and is preferably an expression vector as described below. Retroviral vectors may be replication-competent or replication-defective. In the latter case, viral propagation generally will occur only in complementing host cells.

The polynucleotides may be joined to a vector containing a selectable marker for propagation in a host. Generally, a plasmid vector is introduced into mammalian or avian cells in a precipitate, such as a calcium phosphate precipitate, or in a complex with a charged lipid (e.g., LIPOFECTAMINE™; Life Technologies, Inc.; Rockville, Maryland) or in a complex with a virus (such as an adenovirus; see U.S. Patent Nos. 5,547,932 and 5,521,291) or components of a virus (such as viral capsid peptides). If the vector is a virus, it may be packaged *in vitro* using an appropriate packaging cell line and then transduced into host cells.

Preferred are vectors comprising *cis*-acting control regions to the nucleic acid molecule of interest. Appropriate *trans*-acting factors may be supplied by the

host, by a complementing vector or by the vector itself upon introduction into the host.

In certain preferred embodiments in this regard, the vectors may provide for specific expression of the amplified, synthesized or digested/cleaved nucleic acid molecules, which may be inducible and/or cell type-specific. Particularly preferred among such expression vectors are those inducible by environmental factors that are easy to manipulate, such as temperature and nutrient additives.

Expression vectors useful in the present invention include chromosomal-, episomal- and virus-derived vectors, *e.g.*, vectors derived from bacterial plasmids, bacteriophages, yeast episomes, yeast chromosomal elements, viruses such as baculoviruses, papovaviruses, λ phage, vaccinia viruses, adenoviruses, fowl pox viruses, pseudorabies viruses and retroviruses, and vectors derived from combinations thereof, such as cosmids and phagemids.

In one embodiment, an isolated nucleic acid molecule of the invention or fragment thereof may be operably linked to an appropriate regulatory sequence, preferably a promoter such as the phage lambda PL promoter, promoters from T3, T7 and SP6 phages, the *E. coli lac*, *trp* and *tac* promoters, the SV40 early and late promoters and promoters of retroviral LTRs and derivatives thereof, to name a few. Other suitable promoters will be known to the skilled artisan. The expression constructs will further contain sites for transcription initiation, termination and, in the transcribed region, a ribosome binding site for translation. The coding portion of the mature transcripts expressed by the constructs will preferably include a translation initiation codon (AUG) at the beginning and a termination codon (UAA, UGA or UAG) appropriately positioned at the end of the polypeptide to be translated.

As indicated above, the expression vectors will preferably include at least one selectable marker. Such markers include dihydrofolate reductase (*dhfr*) or neomycin (*neo*) resistance for eukaryotic cell culture and tetracycline (*tet*) or ampicillin (*amp*) resistance genes for culturing in *E. coli* and other bacteria. Representative examples of appropriate hosts include, but are not limited to,

bacterial cells, such as *Escherichia* spp. cells (particularly *E. coli*), *Bacillus* spp. cells (particularly *B. cereus*, *B. subtilis* and *B. megaterium*), *Streptomyces* spp. cells, *Salmonella* spp. cells (particularly *S. typhimurium*) and *Xanthomonas* spp. cells; fungal cells, including yeast cells such as *Saccharomyces* spp. cells; insect cells such as *Drosophila* S2, *Spodoptera* Sf9 or Sf21 cells and *Trichoplusia* High-Five cells; other animal cells (particularly mammalian cells and most particularly human cells) such as CHO, COS, VERO, HeLa, Bowes melanoma cells and HepG2 and other liver cell lines; and higher plant cells. Appropriate culture media and conditions for the above-described host cells are known in the art.

Among vectors preferred for use in bacteria include pQE70, pQE60 and pQE-9, available from Qiagen; pBS vectors, Phagescript vectors, Bluescript vectors, pNH8A, pNH16a, pNH18A and pNH46A, available from Stratagene; pCDNA3 available from Invitrogen; and pGEX, pTrxfus, pTrc99a, pET-5, pET-9, pKK223-3, pKK233-3, pDR540 and pRIT5 available from Pharmacia. Among preferred eukaryotic vectors are pWLNEO, pSV2CAT, pOG44, pXT1, pBK and pSG available from Stratagene; and pSVK3, pBPV, pMSG and pSVL available from Pharmacia. Other suitable vectors will be readily apparent to the skilled artisan.

Among known bacterial promoters suitable for use in the present invention include the *E. coli lacI* and *lacZ* promoters, the T3, T7 and SP6 phage promoters, the *gpt* promoter, the lambda PR and PL promoters and the *trp* promoter. Suitable eukaryotic promoters include the CMV immediate early promoter, the HSV thymidine kinase promoter, the early and late SV40 promoters, the promoters of retroviral LTRs, such as those of the Rous sarcoma virus (RSV), and metallothionein promoters, such as the mouse metallothionein-I promoter.

Introduction of the genetic constructs into the host cells can be effected by a variety of methods, such as calcium phosphate transfection, DEAE-dextran mediated transfection, cationic lipid-mediated transfection, electroporation, transduction, infection, nucleic acid-coated microprojectile bombardment or other

methods. Such methods are described in many standard laboratory manuals, such as Davis *et al.*, *Basic Methods In Molecular Biology* (1986).

Thus, the invention further provides, in an additional embodiment, a method of ligating an amplified nucleic acid molecule into a vector with increased efficiency. Such methods may comprise one or more steps, such as (a) forming a mixture comprising one or more of the above-described nucleic acid molecules and one or more polymerase inhibitors; and (b) ligating the nucleic acid molecules into one or more of the above-described vectors to form one or more genetic constructs. Analogously, the invention also provides methods suitable for cloning a nucleic acid molecule, such as those described above, into one or more of the above-described vectors. An exemplary method may comprise (a) forming a mixture comprising the nucleic acid molecules to be cloned, the cloning vectors and one or more polymerase inhibitors; and (b) ligating the nucleic acid molecules into one or more of the above-described vectors to form one or more genetic constructs. In an additional embodiment, the invention provides a further method of cloning nucleic acid molecules, such as those described above, into one or more vectors comprising: (a) forming a mixture comprising the nucleic acid molecules to be cloned, one or more polymerase inhibitors and one or more of the above-described restriction endonucleases; and (b) ligating the nucleic acid molecules into one or more of the above-described vectors to form one or more genetic constructs. In an additional embodiment, the invention provides a further method of cloning nucleic acid molecules, such as those described above, into one or more vectors comprising: (a) forming a mixture comprising the nucleic acid molecules to be cloned, one or more polymerase inhibitors and one or more of the above-described recombination proteins; and (b) ligating the nucleic acid molecules into one or more of the above-described vectors to form one or more genetic constructs.

According to the invention, the mixture formed in the steps (a) of the above-described methods may further comprise one or more additional components, including but not limited to one or more of the above-described

polypeptides having polymerase activity, one or more dNTPs or ddNTPs, one or more polypeptides having reverse transcriptase activity, one or more buffer salts, and the like. In one of the above aspects of the invention, the polypeptides having polymerase activity and the one or more restriction endonucleases or one or more recombination proteins may be added to the mixture simultaneously. In another of the above aspects, the polymerases and endonucleases or recombinases may be added sequentially, in any order. These methods of the invention may also further comprise one or more additional steps, such as the transformation of one or more of the genetic constructs formed by these methods into one or more of the above-described host cells.

These methods of the invention may be advantageously used to clone or ligate any nucleic acid molecule, which may be an amplified nucleic acid molecule, into a vector and/or host cell. Thus, the invention also provides nucleic acid molecules cloned by such methods, and host cells produced by being transformed with the above-described cloned nucleic acid molecules according to the methods of the invention.

Polymerase Inhibitors

As described above, the methods of the invention (particularly the cloning and ligation methods) advantageously utilize one or more inhibitors of the polymerase activity of the polypeptides used to amplify the nucleic acid molecules. As used herein, an "inhibitor" of a polymerase is defined as any compound, composition or combination thereof that inactivates or reduces the activity of a polypeptide having nucleic acid polymerase activity, reversibly or irreversibly. In particular, inhibitors of a polymerase as used in the present invention will, upon contact with or binding to the polymerase polypeptide, reduce the activity of the polypeptide to no greater than about 70%, 60%, 50%, 40%, 30%, 20%, 10%, 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2% 1% or 0.1%, of the activity of a polypeptide having polymerase activity (such as those described above) that has not been contacted with the inhibitor. As a practical matter, whether a particular inhibitor

reduces the activity to no greater than about 70%, 60%, 50%, 40%, 30%, 20%, 10%, 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2% 1% or 0.1%, of the activity of an uninhibited polypeptide having polymerase activity, may be determined by measuring the unit activity (by the methods described above and others that will be familiar to one of ordinary skill) of the polymerase in the presence and absence of various concentrations of the inhibitor.

A variety of inhibitors are suitable for use in the present methods. Included among these inhibitors are antibodies that bind to the above-described polypeptides having polymerase activity (such as anti-*Taq* antibodies, anti-*Tne* antibodies, anti-*Tma* antibodies or anti-*Pfu* antibodies), and fragments thereof (such as Fab or Fab₂ fragments). Such antibodies may be polyclonal or monoclonal, and may be prepared in a variety of species according to methods that are well-known in the art. See, for instance, Sutcliffe, J.G., *et al.*, *Science* 219:660-666 (1983); Wilson *et al.*, *Cell* 37: 767 (1984); and Bittle, F.J., *et al.*, *J. Gen. Virol.* 66:2347-2354 (1985). Antibodies specific for any of the above-described polymerases, such as anti-*Taq* antibodies, anti-*Tne* antibodies, anti-*Tma* antibodies and anti-*Pfu* antibodies, can be raised against the intact polymerase polypeptide or one or more antigenic polypeptide fragments thereof. These polypeptides or fragments may be presented together with a carrier protein (*e.g.*, albumin) to an animal system (such as rabbit or mouse) or, if they are long enough (at least about 25 amino acids), without a carrier.

As used herein, the term "antibody" (Ab) may be used interchangeably with the terms "polyclonal antibody" or "monoclonal antibody" (mAb), except in specific contexts as described below. These terms, as used herein, are meant to include intact molecules as well as antibody fragments (such as, for example, Fab and F(ab')₂ fragments) which are capable of specifically binding to a polypeptide having polymerase activity (such as a thermostable DNA polymerase or a reverse transcriptase) or a portion thereof.

The anti-polymerase antibodies used in the methods of the present invention may be polyclonal or monoclonal, and may be prepared by any of a

variety of methods (see, e.g., U.S. Patent No. 5,587,287). For example, polyclonal antibodies may be made by immunizing an animal with one or more polypeptides having polymerase activity or portions thereof (e.g., one or more thermostable DNA polymerases such as *Taq*, *Tne*, *Tma* or *Pfu* polymerase) according to standard techniques (see, e.g., Harlow, E., and Lane, D., *Antibodies: A Laboratory Manual*, Cold Spring Harbor, NY: Cold Spring Harbor Laboratory Press (1988); Kaufman, P.B., et al., In: *Handbook of Molecular and Cellular Methods in Biology and Medicine*, Boca Raton, Florida: CRC Press, pp. 468-469 (1995)). Alternatively, anti-polymerase monoclonal antibodies (or fragments thereof), such as anti-DNA polymerase antibodies (e.g., anti-*Taq*, anti-*Tne*, anti-*Tma* or anti-*Pfu* antibodies) to be used in the present methods may be prepared using hybridoma technology that is well-known in the art (Köhler et al., *Nature* 256:495 (1975); Köhler et al., *Eur. J. Immunol.* 6:511 (1976); Köhler et al., *Eur. J. Immunol.* 6:292 (1976); Hammerling et al., In: *Monoclonal Antibodies and T-Cell Hybridomas*, New York: Elsevier, pp. 563-681 (1981); Kaufman, P.B., et al., In: *Handbook of Molecular and Cellular Methods in Biology and Medicine*, Boca Raton, Florida: CRC Press, pp. 444-467 (1995)).

In yet another approach, antibodies capable of binding to one or more polypeptides having polymerase activity, or fragments thereof, may be used to remove the polypeptides having polymerase activity, thus preventing the polymerase from having an adverse effect on cloning of the amplified molecule. In such a procedure, antibodies (or fragments thereof) specific for the polymerase may be used to remove the polymerase from the reaction. Alternatively, the anti-polymerase antibody may be used to inhibit/inactivate the polymerase and a second antibody specific for the anti-polymerase antibody can be used to remove the inactivated polymerase.

It will be appreciated that Fab, F(ab')₂ and other fragments of the above-described antibodies may be used in the methods described herein. Such fragments are typically produced by proteolytic cleavage, using enzymes such as papain (to produce Fab fragments) or pepsin (to produce F(ab')₂ fragments).

Polymerase-binding antibody fragments may also be produced through the application of recombinant DNA technology or through synthetic chemistry.

Alternatively, antibodies directed against one or more of the above-described polypeptides having polymerase activity, which may be used to inhibit the activity of residual polymerases in the reaction mixture following amplification of nucleic acid molecules, may be obtained commercially for example from Life Technologies, Inc. (Rockville, Maryland), Boehringer Mannheim (Indianapolis, Indiana) and Sigma (St. Louis, Missouri).

In addition to antibodies, other compounds that are suitable as inhibitors for use in the present methods include chemicals, which may be synthetic or naturally occurring (such as α -amanitin, polyethylene glycol, dimethylsulfoxide, formamide, dimethylformamide, urea, pyrophosphate, acetic anhydride and diethylpyrocarbonate), antibiotics (such as actinomycin-D), heavy metals (such as compounds containing nickel (particularly Ni^{++} -containing salts) or copper (particularly Cu^{++} -containing salts)), acids (such as digallic acid, aurochloric acid, phosphonoformate and podocypic acid), metal chelators (such as EDTA), nucleotide analogues (such as peptide nucleic acid (PNA) and 2-(*p*-butylanilino)-dATP), sulfhydryl reagents (such as *n*-ethylmaleimide or iodoacetic acid), anionic detergents (such as sodium dodecylsulfate), polyanions (such as spermidine), captan ((*N*-[trichloromethyl]-thio)-4-cyclohexene-1,2-dicarboximide), acidic polysaccharides (such as dextran sulfate and heparin), a binding protein or peptide, and combinations thereof. However, it will be understood by the skilled artisan that any compound, natural or synthetic, that inhibits or inactivates the polymerase activity of a polypeptide according to the above parameters may be advantageously used in the methods of the present invention.

In use, the one or more inhibitors function to increase the efficiency of cloning of the above-described amplified, synthesized or digested nucleic acid molecules. It is thought that such an advantage is due to the action of the inhibitors to prevent or inhibit modification of one or more of the termini (3'

and/or 5') of the amplified, synthesized or digested nucleic acid molecules; it will be understood, however, that regardless of the mechanism of action the one or more inhibitors functions to provide increased efficiency of cloning of the amplified, synthesized and digested nucleic acid molecules.

5 **Compositions**

10 In an another embodiment, the present invention is directed to compositions which may be used, for example, in the methods of the present invention to clone an amplified nucleic acid molecule. Compositions of the invention may comprise one or more components, which may be present in solution or in solid form, and which may be formulated at working concentrations or in solutions of higher concentration (for example, 2X, 2.5X, 5X, 10X, 20X, 25X, 50X, 100X, 250X, 500X, 1000X and the like).

15 A preferred composition of the invention comprises one or more of the above-described restriction endonucleases and one or more of the above-described polymerase inhibitors. These restriction endonucleases and polymerase inhibitors may be present at the working concentrations noted above, or at higher than working concentrations, and may each be present at different concentrations. In particularly preferred compositions of the invention, the restriction endonucleases and polymerase inhibitors are stable upon storage, such that the compositions
20 themselves may be stored for extended periods of time without losing activity. As noted above, the term "stable" as used herein means that the restriction endonucleases and polymerase inhibitors that make up the present compositions retain at least 70%, preferably at least 80%, and most preferably at least 90%, of their original enzymatic activity (in units) after the composition containing the
25 enzyme has been stored for at least four weeks at a temperature of about 20-25°C, at least one year at a temperature of about 4°C or at least 2 years at a temperature of -20°C.

Alternative compositions of the invention may comprise one or more polymerase inhibitors, such as those described above, and may optionally further

comprise one or more additional components, for example, one or more DNA-modifying enzymes or combinations thereof (such as ligases, topoisomerases, kinases, phosphatases, nucleases, endonucleases, terminal deoxynucleotidyl transferases, etc.).

5 The compositions of the invention may additionally comprise one or more nucleic acid molecules (including amplified nucleic acid molecules or fragments or derivatives thereof), one or more nucleotides (including dNTPs, ddNTPs and/or rNTPs), one or more detergents (including TRITON X-100®, Nonidet P-40 (NP-40), Tween 20, Brij 35, sodium deoxycholate or sodium dodecylsulfate), one or
10 more enzyme cofactors and/or one or more suitable buffers (such as TRIS, phosphate salts (such as sodium phosphate (mono- or dibasic) and potassium phosphate), sodium bicarbonate, sodium acetate, HEPES, and the like). Combinations of ammonium sulfate, one or more magnesium salts (such as magnesium chloride or magnesium sulfate), one or more manganese salts (such as
15 manganese sulfate) and potassium chloride (or other salts), may also be used in formulating the compositions of the present invention. A small amount of a salt of ethylenediaminetetraacetate (EDTA) may also be added (preferably about 0.1 millimolar), although inclusion of EDTA does not appear to be essential to the function or stability of the compositions of the present invention. Other
20 components that may advantageously be added to the present compositions to facilitate their use in cloning of amplified nucleic acid molecules will be apparent to the skilled artisan.

 Following formulation, the present compositions may be filtered through a low protein-binding filter unit that is available commercially (for example from
25 Millipore Corporation, Bedford, Massachusetts) and stored until use. To reduce component denaturation, storage of the present compositions is preferably in conditions of diminished light, e.g., in amber or otherwise opaque containers or in storage areas with controlled low lighting. The compositions of the present invention are unexpectedly stable at ambient temperature (about 20°-25°C) for
30 about 4-10 weeks, are stable for at least one year upon storage at 4°C, and for at

least two years upon storage at -20°C . Surprisingly, storage of the compositions at temperatures below freezing (*e.g.*, -20°C to -70°C), as is traditional with stock solutions of bioactive components, is not necessary to maintain the stability of the compositions of the present invention.

5

Kits

10 In another embodiment, the invention relates to kits for cloning an amplified nucleic acid molecule. Kits according to the present invention may comprise a carrier means, such as a box, carton, tube or the like, having in close confinement therein one or more containers, such as vials, tubes, ampules, bottles and the like. A first container in the present kits may contain, for example, one or more of the above-described polymerase inhibitors. The kits of the invention may further comprise one or more additional containers containing one or more additional reagents and compounds, such as one or more polypeptides having polymerase activity, one or more primers, one or more nucleotides (such as dNTPs, ddNTPs and/or rNTPs), one or more polypeptides having reverse transcriptase activity, one or more nucleic acid-modifying enzymes (such as topoisomerases, ligases, phosphatases, etc.), one or more vectors, one or more host cells (particularly one or more of the above-described host cells and most particularly one or more transformation-competent host cells), one or more restriction endonucleases, and one or more recombination proteins. Additional kits of the invention may comprise one or more of the above-described compositions of the invention. These kits and their components are preferably stable upon storage according to the above-described parameters of stability, and may be advantageously used to clone a nucleic acid molecule, preferably an amplified nucleic acid molecule, according to the methods of the invention.

15

20

25

30 It will be readily apparent to one of ordinary skill in the relevant arts that other suitable modifications and adaptations to the methods and applications described herein are obvious and may be made without departing from the scope

of the invention or any embodiment thereof. Having now described the present invention in detail, the same will be more clearly understood by reference to the following examples, which are included herewith for purposes of illustration only and are not intended to be limiting of the invention.

5 **Examples**

Example 1: Inhibition of Polymerase Activity Facilitates Cloning of Amplified Nucleic Acid Molecules

10 In initial experiments, the amount of polymerase activity remaining in a PCR reaction mixture after amplification was determined. The activity of *Taq* DNA polymerase remaining after 30 cycles of PCR was assayed directly by the standard unit assay (Innis, M.A., *et al.*, *Proc. Natl. Acad. Sci. USA* 85:9436-9440 (1988); Gelfand, D.H., in: *Current Communications in Molecular Biology: Polymerase Chain Reaction*, Ehrlich, H., *et al.*, eds., Cold Spring Harbor, New York: Cold Spring Harbor Laboratory, pp. 11-17 (1989)), using several sources of polymerase: Native *Taq* (Life Technologies, Inc.), *Elongase* enzyme mix (Life Technologies, Inc.) and *AmpliTaq* (Perkin-Elmer). The results of these experiments indicated that after 30 cycles of PCR, 60-96% of the initial *Taq* activity remained (data not shown), which was sufficient *Taq* activity to perform another 30 cycles of PCR. These findings therefore confirmed those previously reported (Bennett, B.L., and Molenaar, A.J., *BioTechniques* 16(1):36-37 (1994)).

20 To determine if elimination of this polymerase activity facilitated cloning of the amplification products, a series of experiments was conducted. PCR primers were designed to amplify out a 664-bp fragment within the pPROEX-CAT cloning vector (Life Technologies, Inc.) which encodes a gene for chloramphenicol acetyl transferase (CAT) and confers chloramphenicol resistance

25 on transformants containing the gene. The upstream (5') primer was located near an *EcoRI* site in the CAT coding region and the downstream (3') primer bound to a region 3' to the CAT gene past a unique *HindIII* site. The experiments consisted

of *Taq* polymerase-mediated amplification of the plasmid insert, followed by various methods of *Taq* removal prior to digestion of the termini of the PCR products with *EcoRI* and *HindIII*. Because of extra nucleotide sequence contributions from the primer design, the actual PCR product was 664 bp which generated a 522-bp fragment after digestion. The digested PCR product was then gel purified by electroelution prior to quantitation and ligation into an ampicillin-resistant pPROEX-CAT cloning vector that had been similarly digested with *EcoRI* and *HindIII*. This experimental design therefore provided for direct detection of the number of transformants (*i.e.*, the number of ampicillin-resistant ("amp^r") colonies) and whether the insert was correctly ligated, in-frame, into the vector in these transformants. Specifically, if the insert was correctly ligated, the ampicillin-resistant bacterial colonies would also be resistant to chloramphenicol ("cam^r") in the presence of IPTG, which would induce expression of the CAT gene in the insert. This assay also provided a means of identifying whether the residual *Taq* polymerase had partially or completely filled in the restriction enzyme-generated cohesive ends on the amplicon: partial fill-in of termini by *Taq* prior to ligation would shift the reading frame of the ligated insert and result in improper transcription of the CAT gene and loss of chloramphenicol resistance (*i.e.*, colonies would be observed that were amp^r but not cam^r).

To serve as a positive control for this experiment, the plasmid pPROEX-CAT was digested with *EcoRI* and *HindIII* prior to agarose gel electrophoresis and purification of each of the two generated DNA fragments. The purified vector and insert fragments were religated in a 1:1 molar ratio; this preparation served as a positive control since neither fragment was exposed to *Taq* DNA polymerase. The negative control consisted of a "vector-only" ligation reaction.

The 664-bp fragment was amplified using the pPROEX-CAT vector as a template in a series of amplification reactions such that the total reaction volume was equivalent to 5 ml. After confirmation of successful amplification of the 664-bp fragment by agarose gel analysis and EtBr-staining, all of the reactions were pooled to minimize sample variation that may have taken place during PCR which

could potentially bias the cloning results. This pool was then resplit into several aliquots to undergo post-PCR manipulations, designed to reduce or eliminate residual *Taq* polymerase prior to cloning, as follows:

- 5 **a.) Ethanol precipitation:** A 600 µl aliquot of the reaction pool was precipitated with ethanol in the presence of sodium acetate, followed by digestion of the precipitate with *Eco*RI and *Hind*III in React 2 buffer. Following RE-digestion, the sample was extracted once with phenol/chloroform/isoamyl alcohol (25:24:1) followed by an additional 100% chloroform extraction. The sample was then subjected to electrophoresis on a 1% agarose gel, followed by EtBr staining and excision of the 564-bp fragment. The DNA was recovered from the gel slice by electroelution, ethanol precipitated again, resuspended in TE buffer or sterile water and then a portion of it was visually quantitated on an agarose gel by EtBr-staining compared to similarly stained standards.
- 10
- 15 **b.) Gel Purification:** A 600 µl aliquot of the PCR pool was subjected to agarose-gel electrophoresis and EtBr-staining and was recovered from the gel by using a GlassMAX procedure according to the manufacturer's instructions (Life Technologies, Inc.). The recovered DNA fragment was digested with *Eco*RI and *Hind*III as described above, and subjected to a second round of gel purification as described above using electroelution and subsequent visual quantitation.
- 20 **c.) Phenol/chloroform extraction:** A 600 µl aliquot of the PCR pool was extracted twice using an equal volume of phenol/chloroform (49:1) followed by ethanol precipitation in the presence of sodium acetate. The precipitate was then digested, purified by electrophoresis, ethanol precipitated and visually quantitated as described above.

- 25 **d.) Anti-Taq Antibody treatment:** A 600 µl aliquot of the PCR pool was added to 6 µl of TaqStart antibody (CloneTech). Per the manufacturer's

recommendations, this was an appropriate amount of antibody to inactivate 25-30 units of *Taq*, the amount that was initially present in the amplification reaction mixture. The reaction was incubated at about 20-25°C for 40 minutes to allow the antibody to bind to the *Taq* enzyme. Following this incubation, the reaction mix was digested with *Eco*RI and *Hind*III in React 2 buffer and then ethanol precipitated as above. The sample was then subjected to agarose gel electrophoresis, electroelution and visual quantitation as described above.

Following these various treatments and visual quantitation of the resulting inserts, the inserts were ligated into the pPROEX-CAT vector. Ligation reactions were set up at a 1:1 (10 ng insert:100 ng vector) molar ratio, and incubated for 12-18 hours at 12°C using T4 DNA ligase in a 20 µl volume. The reactions were then diluted to 100 µl of sterile water, and 5 µl of this dilution were added to 100 µl of transformation-competent DH10B *E. coli* cells (Life Technologies, Inc.). Following transformation, various dilutions of the reaction (1 ml each) were plated out on LBamp and LBcam/IPTG plates (Life Technologies, Inc.) to determine the numbers of recombinant (amp^r) and CAT-expressing (cam^r) colonies. Results are shown in Table 1.

Table 1. *Effect of Taq Removal on Cloning Efficiency.*

Post-PCR treatment	Cloning Efficiency Number of Amp ^r colonies	Correct Recombinants % Cam ^r (No. of Colonies)
vector-only (neg. control)	13	7 (1)
vector+insert religation (pos. control)	4250	84 (3550)
<i>Taq</i> Antibody treatment	1500	85 (1275)
Ethanol precipitation	700	22 (154)
Gel Purification	495	100 (495)
Phenol/chloroform extraction	2350	96 (2256)

The results shown in Table 1 demonstrate that treatment of the PCR sample with anti-*Taq* antibody prior to restriction enzyme digestion resulted in a high number of transformants (amp^r colonies), with a large proportion (85%) of these being cam^r indicating that the correct reading frame was maintained during ligation. These results compare favorably with the positive control and also with the phenol/chloroform extraction method, which has been shown previously to result in higher post-PCR cloning efficiencies (Bennett, B.L., and Molenaar, A.J., *BioTechniques* 16(1):36-37 (1994), and which has heretofore been the method of choice for reducing residual *Taq* activity. Ethanol precipitation of the PCR product followed by digestion and purification resulted in a reduced number of cam^r colonies, consistent with previous reports that ethanol precipitation is insufficient to remove residual *Taq* DNA polymerase activity (Bennett, B.L., and Molenaar, A.J., *BioTechniques* 16(1):36-37 (1994). Gel purification of the PCR product to remove *Taq* DNA polymerase prior to RE-digestion resulted in 100% of the amp^r recombinants being cam^r, but the overall number of transformants were the lowest compared to the other treatment groups. Furthermore, this double gel purification was the most time-consuming and inefficient method since

it resulted in large losses of amplification product due to the manipulations involved in two successive rounds of agarose gel purification.

Together, these data indicate that it is advantageous to use a *Taq* antibody to facilitate post-PCR cloning of amplified nucleic acid molecules. Such an approach increases the efficiency and yield of clones obtained from amplified nucleic acid molecules, both by decreasing the number of experimental manipulations that are used and by obviating the use of potentially harmful organic solvents (phenol/chloroform) for extraction of residual *Taq* activity.

Example 2: Radioactive Assay of Efficiency of Cloning of Amplified Nucleic Acid Molecules

To confirm the above results in a more sensitive assay, a radioactive method was employed. A 664-bp amplicon, which encodes the 3' end of the chloramphenicol acetyl transferase (CAT) gene, was amplified using *Taq* DNA polymerase (5 units/100 μ l) and the primers detailed in Example 1. For set-up of the radioactive assay, the amplification product (5 μ l containing 0.25 units of *Taq* DNA polymerase at the start of PCR) was incubated in the presence and absence of two different preparations of anti-*Taq* antibodies ("antibody #1" and "antibody #2"; Life Technologies, Inc. (Rockville, Maryland)), for 15 minutes at room temperature (20-25°C) prior to digestion with *Eco*RI and *Hind*III at 37°C for one hour. Along with the restriction enzymes, 20 uCi of 32 P-dATP was added to each reaction to monitor potential fill-in of 3'-recessed termini by residual *Taq* DNA polymerase. As an additional positive control, three units of Klenow fragment were added to one reaction to examine maximal incorporation of nucleotides. Replicate samples were spotted in duplicate onto glass fiber filters followed by precipitation of incorporated nucleotides in the presence of ice cold 10% TCA/0.1% pyrophosphate.

The results of these experiments are shown Table 2.

Table 2. *Effects of Anti-Taq Antibodies on 3' Terminal Fill-in*

	Treatment Before RE Digestion	Incorporation (cpm; replicates)
5	TCA precipitation blank (negative control)	588, 976
	none	7521, 7811, 7182, 6868
	RE digestion followed by Klenow treatment (positive control)	51271, 53619
	Antibody #1, 1 unit	896, 664
	Antibody #1, 0.67 units	598, 660
10	Antibody #1, 0.33 units	732, 696
	Antibody #2, 1 unit	600, 602
	Antibody #2, 0.67 units	472, 536
	Antibody #2, 0.33 units	670, 956

These results indicate that *Taq* DNA polymerase does, indeed, catalyze the incorporation of nucleotides into TCA-precipitable material. Both antibody formulations inhibited incorporation of TCA-precipitable counts to approximately background (blank) levels.

To determine if these cpm were incorporated into the clonable fragment, the samples were subjected to agarose-gel electrophoresis followed by autoradiography. As shown in Figure 1, radiolabel was incorporated into the 522-bp band in samples that were not preincubated with the antibody prior to restriction enzyme digestion. The intensity of this 522-bp band on the x-ray film was greatly diminished in all samples that were incubated with *Taq* antibody prior to digestion, in support of the data shown above in Table 2.

Together, these results indicate that inclusion of anti-*Taq* antibodies in the reaction mixture prevents the residual polymerase activity from filling in the 3' recessed termini in restriction enzyme-digested amplified nucleic acid molecules.

Example 3: Cloning of Amplified Nucleic Acid Molecules

A 664-bp amplicon was amplified using *Taq* DNA polymerase (5 units/100µl) as described in Example 1. 50 µl of the amplification reaction (2.5

units of *Taq* DNA polymerase) were removed and incubated with 3.3 units (10 μ l) of anti-*Taq* antibody (Life Technologies, Inc.; Rockville, Maryland) for seven minutes at room temperature (about 20-25°C). Two additional 50 μ l aliquots were incubated with 10 μ l of antibody dilution buffer to serve as the control reactions. Following this preincubation, all three reactions were incubated with 60 units each of *Eco*RI and *Hind*III in a total volume of 120 μ l in React-2 buffer for one hour at 37°C. Five units of Klenow enzyme were added to one of the control reactions and incubated for an additional 10 minutes at 37°C to examine how filling in the 3' recessed ends of the digested amplicon affects the number of colonies obtained in a cloning experiment. All three reactions mixtures were ethanol precipitated and subjected to agarose gel electrophoresis and the 522-bp clonable DNA was gel purified using GlassMax as described in Example 1. Following purification, the concentration of the three different insert preparations was determined using a Kodak Digital Imaging Camera so that equivalent amounts of the purified 522-bp insert were added to each ligation reaction.

The three inserts were each ligated into gel-purified pPROEXCAT that had been digested with *Eco*RI and *Hind*III. One tenth of the ligation was transformed into DH5 α subcloning-competent *E. coli* cells (Life Technologies, Inc.), and the transformations were plated in triplicate onto LB plates containing 100 μ g/ml ampicillin and X-gal, and onto LB plates containing 100 μ g/ml ampicillin, 7.5 μ g/ml chloramphenicol, X-gal and IPTG. The chloramphenicol/IPTG platings were performed to assess the percentage of *cam*^r recombinants, as an indication of the number of in-frame ligations as described above. Results are shown in Table 3.

Table 3. *Efficiency of Cloning of Amplified Nucleic Acid Molecules.*

<i>Sample</i>	<i>No. of amp^r colonies</i>	<i>No. of cam^r colonies</i>
vector-only (neg. control)	17	16
Klenow fill-in (pos. control)	155	31
no antibody	28	48
anti- <i>Taq</i> antibody	1317	932
insert only (neg. control)	0	nd*

*nd = not determined

These results demonstrate that the addition of *Taq* antibody to the reaction, prior to restriction enzyme-mediated generation of 3' recessed termini, augments the efficiency of cloning of the amplified inserts. Based on these findings, it is therefore desirable to add a polymerase inhibitor, such as an anti-*Taq* antibody, to the reaction mixture prior to digestion of PCR products with restriction enzymes, in order to increase the efficiency of cloning of the amplified nucleic acid molecules.

Example 4: *Simultaneous Treatment of Amplified Nucleic Acid Molecules with Anti-*Taq* Antibodies and Restriction Enzymes*

The results shown in Example 3 indicate that sequential addition of polymerase inhibitors and restriction endonucleases greatly increases the efficiency of cloning of amplified nucleic acid molecules. To determine if this sequential addition of these reagents was necessary, the cloning experiments described in Example 3 were repeated, except that the anti-*Taq* antibody was added to the reaction simultaneously with the *Eco*RI and *Hind*III restriction enzymes (*i.e.*, no preincubation, as in Example 3, was performed). In addition, a 1:1 ratio of *Taq* and anti-*Taq* antibody (per the unit definition of the antibody noted above) was employed; all other experimental techniques were the same as in Example 3.

Results of these experiments are shown in Table 4.

Table 4. *Simultaneous Addition of Antibody and Restriction Enzymes.*

Sample Treatment	No. of amp ^r colonies	No. of cam ^r colonies
vector-only (neg. control)	4	5
Klenow fill-in (pos. control)	9	7
no antibody	10	8
anti- <i>Taq</i> antibody	741	520
pUC 19 transformation control*	30	0

*Transformation/plating control to demonstrate no growth on the chloramphenicol plates with a vector which cannot support CAT expression. Not corrected back to transformation efficiency (cfu/μg).

These results confirm those of Example 3, indicating that treatment of the amplification reaction mixture with a polymerase inhibitor, such as an anti-*Taq* antibody, increases the efficiency of cloning of the amplified nucleic acid molecules. More importantly, these results indicate that the polymerase inhibitors and the restriction endonucleases may be added to the reaction mixture simultaneously or sequentially, with equivalent results.

Example 5: Reduction of *Taq* DNA Polymerase-mediated Artifacts by Treatment of PCR Reactions with Anti-*Taq* Antibodies

When T/A cloning is performed, amplified nucleic acid is mixed (without purification) with the cloning vector and then ligation is performed and host cells transformed. The efficiency of this cloning method can be extremely variable. One parameter affecting efficiency is the stability of the vector which has 3' dT overhangs that are needed to get specific annealing with the amplified product. In order to investigate the effect of *Taq* and other components of the PCR reaction on the vector itself during ligation, the following experiment was done. A mock PCR reaction was prepared that contained all the components of a normal reaction except template and primers. Thirty cycles of amplification were performed, and an aliquot of this PCR reaction which was equivalent to that

normally used was added to the vector either with or without anti-*Taq* antibodies (obtained from Life Technologies, Inc.; Rockville, Maryland). The ligation reaction and transformation were then performed according to the manufacturer's instructions (Invitrogen). The screen for transformants in this system was a determination of the lack of LacZ α complementation (presence of white colonies) as described in Sambrook, J., *et al.*, *Molecular Cloning, A Laboratory Manual*, 2nd ed., Cold Spring Harbor, New York: Cold Spring Harbor Laboratory (1989). In an ideal situation, there should be no colonies of any kind with the vector alone in the ligation; typically, however, there a very small number of background colonies are observed (*i.e.*, 1-5 white colonies and 2-20 blue colonies). White colonies result when the expression of the LacZ α is stopped by insertion of an amplified product, or in this case by some other mechanism (for example, exonuclease contamination that chews back the ends of the vector). Blue colonies are presumed to arise from religation of the vector that has lost the 3' dT overhang and is religated resulting in the expression of the α peptide.

As shown in Table 5, the presence of untreated *Taq* DNA polymerase (in the PCR reaction mixtures) in the samples containing ligated vector alone resulted in dramatically increased background (white/green colonies). This background was reduced substantially in the samples that were treated with anti-*Taq* antibody prior to ligation.

Table 5. *Reduction of Taq-mediated Cloning Artifacts Using Anti-Taq Antibodies*

Sample	No. of White Colonies	No. of Blue Colonies
Vector + <i>Taq</i> (PCR reaction)	41, 122	30, 13
Vector + <i>Taq</i> (PCR reaction) + antibody	1, 4	2, 42
Vector alone	1, 0	2, 24

These results indicate that *Taq* may have a deleterious effect on the vector (e.g., modifying the 3' and/or 5' termini) and may account for the large variability in efficiency seen with T/A cloning. Reduction of this artifact, for example by use of anti-*Taq* antibody according to the methods of the present invention, leads to decreased background (lower number of colonies) and reduced variation in cloning efficiency.

Having now fully described the present invention in some detail by way of illustration and example for purposes of clarity of understanding, it will be obvious to one of ordinary skill in the art that the same can be performed by modifying or changing the invention within a wide and equivalent range of conditions, formulations and other parameters without affecting the scope of the invention or any specific embodiment thereof, and that such modifications or changes are intended to be encompassed within the scope of the appended claims.

All publications, patents and patent applications mentioned in this specification are indicative of the level of skill of those skilled in the art to which this invention pertains, and are herein incorporated by reference to the same extent as if each individual publication, patent or patent application was specifically and individually indicated to be incorporated by reference.

WHAT IS CLAIMED IS:

1. A method of cloning an amplified or synthesized nucleic acid molecule, comprising:

(a) amplifying or synthesizing one more nucleic acid molecules
5 in the presence of one or more polypeptides having polymerase activity to produce amplified nucleic acid molecules; and

(b) incubating said amplified or synthesized nucleic acid molecules with one or more inhibitors of the polypeptides having polymerase activity under conditions sufficient to inhibit or inactivate the polymerase activity.

10 2. The method of claim 1, further comprising digesting said amplified or synthesized nucleic acid molecules with one or more restriction endonucleases, to produce digested nucleic acid molecules.

15 3. The method of claim 2, further comprising ligating said digested nucleic acid molecules into one or more vectors to form one or more genetic constructs.

20 4. The method of claim 1, further comprising ligating said amplified or synthesized nucleic acid molecules into one or more vectors to form one or more genetic constructs.

5. The method of claim 3 or claim 4, further comprising transforming said one or more genetic constructs into one or more host cells.

25 6. The method of claim 1, wherein the inhibition or inactivation of said polypeptides having polymerase activity increases the efficiency of cloning of said amplified or synthesized nucleic acid molecules into one or more vectors.

7. The method of claim 2, wherein the inhibition or inactivation of said polypeptides having polymerase activity increases the efficiency of cloning of said digested nucleic acid molecules into one or more vectors.

5 8. The method of claim 1, wherein said inhibitors prevent or inhibit modification of one or more termini of said amplified or synthesized nucleic acid molecules.

10 9. The method of claim 2, wherein said inhibitors prevent or inhibit modification of one or more termini of said digested nucleic acid molecules.

10. The method of claim 1, wherein said inhibitors allow increased efficiency of cloning of said amplified or synthesized nucleic acid molecules into one or more vectors.

15 11. The method of claim 2, wherein said inhibitors allow increased efficiency of cloning of said digested nucleic acid molecules into one or more vectors.

20 12. The method of claim 1, wherein said amplification or synthesis comprises:

(a) contacting a first nucleic acid molecule, a first primer molecule which is complementary to a portion of said first nucleic acid molecule, a second nucleic acid molecule and a second primer molecule which is complementary to a portion of said second nucleic acid molecule, with one or more polypeptides having polymerase activity;

25 (b) incubating said molecules under conditions sufficient to form a third nucleic acid molecule complementary to all or a portion of said first nucleic acid molecule and a fourth nucleic acid molecule complementary to all or a portion of said second nucleic acid molecule;

30

- (c) denaturing said first and third and said second and fourth nucleic acid molecules; and
- (d) repeating steps (a) through (c) one or more times.

13. The method of claim 1, wherein said polypeptides are selected from
5 the group consisting of DNA polymerases and reverse transcriptases.

14. The method of claim 13, wherein said polypeptides are
thermostable DNA polymerases.

10 15. The method of claim 13, wherein said polypeptides are selected
from the group consisting of *Taq* DNA polymerase, *The* DNA polymerase, *Tma*
DNA polymerase, *Pfu* DNA polymerase, *Tfi* DNA polymerase, *Th* DNA
polymerase, *Pwo* DNA polymerase, VENT™ DNA polymerase, DEEPVENT™
DNA polymerase, T7 DNA polymerase, T5 DNA polymerase, DNA
15 polynierase III, Klenow fragment DNA polymerase, Stoffel fragment DNA
polymerase, and mutants, fragments or derivatives thereof.

16. The method of claim 13, wherein said polypeptides are selected
from the group consisting of M-MLV reverse transcriptase, RSV reverse
20 transcriptase, AMV reverse transcriptase, RAV reverse transcriptase, MAV
reverse transcriptase, HIV reverse transcriptase, M-MLV H reverse transcriptase,
RSV H⁻ reverse transcriptase, AMV H⁻ reverse transcriptase, RAV H⁻ reverse
transcriptase, MAVH⁻ reverse transcriptase and HIVH⁻ reverse transcriptase, and
mutants, fragments or derivatives thereof.

25

17. The method of claim 13, wherein said DNA polypeptide is *The*
DNA polymerase or a mutant, fragment or derivative thereof.

18. The method of claim 13, wherein said polypeptide is *Tma* DNA polymerase or a mutant, fragment or derivative thereof.

5 19. The method of claim 13, wherein said polypeptide is *Taq* DNA polymerase or a mutant, fragment or derivative thereof.

20. The method of claim 13, wherein said polypeptide is a T7 DNA polymerase or a mutant, fragment or derivative thereof.

10 21. A method of ligating an amplified or synthesized nucleic acid molecule into a vector with increased efficiency, comprising:

- 15 (a) forming a mixture comprising said amplified or synthesized nucleic acid molecules and one or more polymerase inhibitors; and
(b) ligating said nucleic acid molecules into one or more vectors to form one or more genetic constructs.

22. The method of claim 21, wherein said mixture further comprises one or more polypeptides having polymerase activity.

20 23. The method of claim 21, further comprising transforming said one or more genetic constructs into one or more host cells.

24. A method for cloning one or more nucleic acid molecules into one or more vectors, comprising:

- 25 (a) forming a mixture comprising said nucleic acid molecules to be cloned, said vectors and one or more polymerase inhibitors; and
(b) ligating said nucleic acid molecules into said vectors to form one or more genetic constructs.

25. The method of claim 24, wherein said mixture further comprises one or more polypeptides having polymerase activity.

5 26. The method of claim 24, wherein said nucleic acid molecules to be cloned are amplified or synthesized nucleic acid molecules.

27. The method of claim 24, further comprising transforming said one or more genetic constructs into one or more host cells.

10 28. A method for cloning one or more nucleic acid molecules into one or more vectors, comprising:

(a) forming a mixture comprising said nucleic acid molecules to be cloned, one or more polymerase inhibitors and one or more restriction endonucleases; and

15 (b) ligating said nucleic acid molecules into one or more vectors to form one or more genetic constructs.

20 29. The method of claim 28, wherein said mixture further comprises one or more polypeptides having polymerase activity.

30. The method of claim 28, wherein said nucleic acid molecules to be cloned are amplified or synthesized nucleic acid molecules.

25 31. The method of claim 28, further comprising transforming said one or more genetic constructs into one or more host cells.

32. The method of claim 28, wherein said inhibitors and said restriction endonucleases are added simultaneously.

33. The method of claim 28, wherein said inhibitors and said restriction endonucleases are added sequentially.

34. The method of any one of claims 1, 21, 24 or 28, wherein said one or more inhibitors are selected from the group consisting of an antibody or a fragment thereof, a chemical compound, an antibiotic, a heavy metal, an acid, a metal chelator, a nucleotide analogue, a sulfhydryl reagent, an anionic detergent, a polyanion, captan ((N-[trichloromethyl]-thio)-4-cyclohexene-1,2-dicarboximide), an acidic polysaccharide, a binding protein or peptide, and combinations thereof.

35. The method of claim 34, wherein said inhibitor is an antibody or fragment thereof.

36. The method of claim 35, wherein said antibody or fragment thereof is selected from the group consisting of an anti-*Taq* antibody, an anti-*The* antibody, an anti-*Tma* antibody, an anti-*Pfu* antibody and fragments thereof.

37. A kit for cloning an amplified or synthesized nucleic acid molecule comprising one or more polymerase inhibitors.

38. The kit of claim 37, wherein said one or more inhibitors are selected from the group consisting of an antibody or a fragment thereof, a chemical compound, an antibiotic, a heavy metal, an acid, a metal chelator, a nucleotide analogue, a sulfhydryl reagent, an anionic detergent, a polyanion, captan ((N-[trichloromethyl]-thio)-4-cyclohexene-1,2-dicarboximide), an acidic polysaccharide, a binding protein or peptide, and combinations thereof.

39. The kit of claim 38, wherein said inhibitor is an antibody or fragment thereof.

40. The kit of claim 39, wherein said antibody is selected from the group consisting of an anti-*Taq* antibody, an anti-*The* antibody, an anti-*Tma* antibody, an anti-*Pfu* antibody and fragments thereof.

5 41. The kit of claim 37, further comprising one or more polypeptides having polymerase activity.

10 42. The kit of claim 37, wherein said kit comprises one or more components selected from the group consisting of one or more primers, one or more nucleotides, one or more polypeptides having polymerase activity, one or more polypeptides having reverse transcriptase activity, one or more ligases, one or more topoisomerases, one or more vectors, one or more host cells, and one or more restriction endonucleases.

15 43. The kit of claim 42, wherein said host cells are competent for transformation.

20 44. A nucleic acid molecule produced by the method of any one of claims 1, 3 or 4.

45. A composition comprising one or more restriction endonucleases and one or more polymerase inhibitors.

25 46. The composition of claim 45, wherein said one or more inhibitors are selected from the group consisting of an antibody or a fragment thereof, a chemical compound, an antibiotic, a heavy metal, an acid, a metal chelator, a nucleotide analogue, a sulfhydryl reagent, an anionic detergent, a polyanion, captan ((N-[trichloromethyl]-thio)-4-cyclohexene-1,2-dicarboximide), an acidic polysaccharide, a binding protein or peptide, and combinations thereof.

47. The composition of claim 46, wherein said inhibitor is an antibody or fragment thereof.

5 48. The composition of claim 47, wherein said antibody is selected from the group consisting of an anti-*Taq* antibody, an anti-*Tne* antibody, an anti-*Tma* antibody, an anti-*Pfu* antibody and fragments thereof.

49. The composition of claim 45, wherein said restriction endonucleases and/or polymerase inhibitors are stable upon storage.

10 50. The composition of claim 45, further comprising one or more polypeptides having polymerase activity.

51. The composition of claim 45, further comprising one or more nucleic acid molecules.

15 52. The composition of claim 45, further comprising one or more buffers.

Methods and Compositions for Cloning Nucleic Acid Molecules

ABSTRACT

5 The present invention is directed generally to methods facilitating the
cloning of nucleic acid molecules. In particular, the invention relates to the use
of polymerase inhibitors, including but not limited to anti-polymerase antibodies
(such as anti-*Taq* antibodies) and fragments thereof, to inactivate residual
polymerase activity remaining after the amplification (particularly via PCR) of a
target nucleic acid molecule. The invention further provides compositions,
10 particularly storage-stable compositions, comprising one or more components,
such as one or more restriction endonucleases and one or more polymerase
inhibitors, that are useful in cloning amplified or synthesized nucleic acid
molecules by the above-described methods. The invention also relates to nucleic
acid molecules produced by these methods, and to genetic constructs (such as
15 vectors) and host cells comprising these nucleic acid molecules.

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:

FOX *et al.*

Appl. No. (To be assigned; Divisional of
Appl. No. 09/134,672)

Filed: HERewith (October 27, 2000)

For: **Methods and Compositions for
Cloning Nucleic Acid Molecules**

Art Unit: To be assigned

Examiner: To be assigned

Atty. Docket: 0942.4460002/RWE/BJD

30813 U.S. PTO
09/697079
10/27/00

Letter to PTO Draftsman: Submission of Formal Drawings

Commissioner for Patents
Washington, D.C. 20231

Sir:

Submitted herewith is one sheet of formal drawing with Figure 1, corresponding to the informal drawing submitted with the above-captioned application. The application number, group art unit and attorney docket number appear on the back of the sheet. Acknowledgment of the receipt, approval, and entry of the formal drawing into this application is respectfully requested.

It is not believed that an extension of time is required, other than any already provided herewith. However, if an extension of time is needed to prevent abandonment of the application, then such extension of time is hereby petitioned. The U.S. Patent and Trademark Office is hereby authorized to charge any fee deficiency, or credit any overpayment, to our Deposit Account No. 19-0036. A duplicate copy of this Letter is enclosed.

Respectfully submitted,

STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.



Brian J. Del Buono
Agent for Applicants
Registration No. 42,473

Date: Oct. 27, 2000

1100 New York Avenue, N.W.
Suite 600
Washington, D.C. 20005-3934
(202) 371-2600

00697079.102700

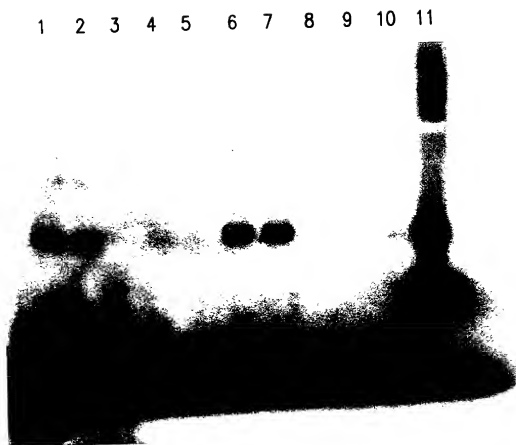


FIG.1

Declaration for Patent Application

Docket Number: 0942.4460001

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name.

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter that is claimed and for which a patent is sought on the invention entitled Methods and Compositions for Cloning Amplified Nucleic Acid Molecules, the specification of which is attached hereto unless the following box is checked:

- ☒ was filed on August 14, 1998;
as United States Application Number or PCT International Application Number 09/134,672; and
was amended on _____ (if applicable).

I hereby state that I have reviewed and understand the contents of the above identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose information that is material to patentability as defined in 37 C.F.R. § 1.56.

I hereby claim foreign priority benefits under 35 U.S.C. § 119(a)-(d) or § 365 (b) of any foreign application(s) for patent or inventor's certificate, or § 365(a) of any PCT international application, which designated at least one country other than the United States listed below, and have also identified below any foreign application for patent or inventor's certificate, or PCT international application having a filing date before that of the application on which priority is claimed.

Prior Foreign Application(s)

Priority Claimed

(Application No.)

(Country)

(Date/Month/Year/Filed)

☐ Yes ☐ No

(Application No.)

(Country)

(Date/Month/Year/Filed)

☐ Yes ☐ No

I hereby claim the benefit under 35 U.S.C. § 119(e) of any United States provisional application(s) listed below.

60/055,849
(Application No.)

August 15, 1997
(Filing Date)

(Application No.)

(Filing Date)

I hereby claim the benefit under 35 U.S.C. § 120 of any United States application(s), or under § 365(c) of any PCT international application designating the United States, listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT international application in the manner provided by the first paragraphs of 35 U.S.C. § 112, I acknowledge the duty to disclose information that is material to patentability as defined in 37 C.F.R. § 1.56 that became available between the filing date of the prior application and the national or PCT international filing date of this application.

(Application No.)

(Filing Date)

(Status-patented, pending, abandoned)

(Application No.)

(Filing Date)

(Status-patented, pending, abandoned)

Send Correspondence to:

STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
1100 New York Avenue, N.W.
Suite 600
Washington, D.C. 20005-3934

Direct Telephone Calls to:

(202) 371-2600

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

Full name of sole or first inventor	Fox, Donna K.	
Inventor's signature	<i>Donna K. Fox</i>	Date 9/16/98
Residence	7407 Village Road, #25, Sykesville, Maryland 21784	
Citizenship	U.S.A.	
Post Office Address	Same as residence	
Full name of second inventor	Chatterjee, Deb K.	
Second Inventor's signature	<i>Deb K. Chatterjee</i>	Date 9/17/98
Residence	6 Forest Ridge Ct., North Potomac, Maryland 20878	
Citizenship	U.S.A.	
Post Office Address	same as residence	

SCANNED. # 22